



Sequence Listing

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Botstein, David  
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Eaton, Dan  
Ferrara, Napoleon  
Filvaroff, Ellen  
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Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Hillan, Kenneth J  
Kljavin, Ivar J.  
Kuo, Sophia S.  
Napier, Mary A.  
Pan, James;  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Shelton, David L.  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William I.

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Met	Val	Lys	Phe	Pro	Ala	Leu	Thr	His	Tyr	Trp	Pro	Leu	Ile	Arg	1	5	10	15
Phe	Leu	Val	Pro	Leu	Gly	Ile	Thr	Asn	Ile	Ala	Ile	Asp	Phe	Gly	20	25	30	
Glu	Gln	Ala	Leu	Asn	Arg	Gly	Ile	Ala	Ala	Val	Lys	Glu	Asp	Ala	35	40	45	
Val	Glu	Met	Leu	Ala	Ser	Tyr	Gly	Leu	Ala	Tyr	Ser	Leu	Met	Lys	50	55	60	
Phe	Phe	Thr	Gly	Pro	Met	Ser	Asp	Phe	Lys	Asn	Val	Gly	Leu	Val	65	70	75	
Phe	Val	Asn	Ser	Lys	Arg	Asp	Arg	Thr	Lys	Ala	Val	Leu	Cys	Met	80	85	90	
Val	Val	Ala	Gly	Ala	Ile	Ala	Ala	Val	Phe	His	Thr	Leu	Ile	Ala	95	100	105	
Tyr	Ser	Asp	Leu	Gly	Tyr	Tyr	Ile	Ile	Asn	Lys	Leu	His	His	Val	110	115	120	
Asp	Glu	Ser	Val	Gly	Ser	Lys	Thr	Arg	Arg	Ala	Phe	Leu	Tyr	Leu	125	130	135	
Ala	Ala	Phe	Pro	Phe	Met	Asp	Ala	Met	Ala	Trp	Thr	His	Ala	Gly	140	145	150	
Ile	Leu	Leu	Lys	His	Lys	Tyr	Ser	Phe	Leu	Val	Gly	Cys	Ala	Ser	155	160	165	
Ile	Ser	Asp	Val	Ile	Ala	Gln	Val	Val	Phe	Val	Ala	Ile	Leu	Leu	170	175	180	
His	Ser	His	Leu	Glu	Cys	Arg	Glu	Pro	Leu	Leu	Ile	Pro	Ile	Leu	185	190	195	
Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu	200	205	210	

Gly Tyr Tyr Lys	Asn Ile His Asp Ile	Ile Pro Asp Arg Ser	Gly
	215	220	225
Pro Glu Leu Gly	Gly Asp Ala Thr Ile	Arg Lys Met Leu Ser	Phe
	230	235	240
Trp Trp Pro Leu	Ala Leu Ile Leu Ala	Thr Gln Arg Ile Ser	Arg
	245	250	255
Pro Ile Val Asn	Leu Phe Val Ser Arg	Asp Leu Gly Gly Ser	Ser
	260	265	270
Ala Ala Thr Glu	Ala Val Ala Ile Leu	Thr Ala Thr Tyr Pro	Val
	275	280	285
Gly His Met Pro	Tyr Gly Trp Leu Thr	Glu Ile Arg Ala Val	Tyr
	290	295	300
Pro Ala Phe Asp	Lys Asn Asn Pro Ser	Asn Lys Leu Val Ser	Thr
	305	310	315
Ser Asn Thr Val	Thr Ala Ala His Ile	Lys Lys Phe Thr Phe	Val
	320	325	330
Cys Met Ala Leu	Ser Leu Thr Leu Cys	Phe Val Met Phe Trp	Thr
	335	340	345
Pro Asn Val Ser	Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val	Asp
	350	355	360
Phe Ala Phe Ala	Glu Leu Cys Val Val	Pro Leu Arg Ile Phe	Ser
	365	370	375
Phe Phe Pro Val	Pro Val Thr Val Arg	Ala His Leu Thr Gly	Trp
	380	385	390
Leu Met Thr Leu	Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser	Val
	395	400	405
Leu Arg Ile Ile	Val Leu Ile Ala Ser	Leu Val Val Leu Pro	Tyr
	410	415	420
Leu Gly Val His	Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu	Ala
	425	430	435
Gly Phe Val Gly	Glu Ser Thr Met Val	Ala Ile Ala Ala Cys	Tyr
	440	445	450
Val Tyr Arg Lys	Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala	Thr
	455	460	465
Glu Gly Glu Asp	Ser Ala Met Thr Asp	Met Pro Pro Thr Glu	Glu
	470	475	480
Val Thr Asp Ile	Val Glu Met Arg Glu	Glu Asn Glu	
	485	490	

<210> 8  
<211> 535  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 66, 96, 387  
<223> unknown base

<400> 8  
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50  
tgagcttctg gtgcennttg gctctaattc tggccacaca gagaancagt 100  
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250  
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
ggccacatc aagaagttca ctttctctg catggctctg tcaactcacgc 350  
tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400  
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450  
gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500  
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9  
<211> 434  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,  
293, 296, 305, 336, 358, 361  
<223> unknown base

<400> 9  
tgacggaatc ccgggctggg tctcctggt tngacaagat aaacccccag 50  
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100  
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttctgtgat 150  
gttttgagaca ccaaagtgt ttgagaaaat tttgatagac atnatcggag 200  
tggantttgc ctttgacagaa ntttgngntg ttcctttgcg gattttctcc 250  
tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350  
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400  
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10  
<211> 154  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 49, 68, 83, 90, 98, 119  
<223> unknown base

<400> 10  
tattcccatg tccggtcacg gggagggcgc atntcaccgg gtggctgang 50  
aactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100  
cgtcctcatc gccagcctng tggtcctacc ctacctgggg gtgcacggtg 150  
agac 154

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgtcac tcacgctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcattcttc cctctccc 18

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccttccgcca cggagttc 18

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
ggcaaagtcc actccgatga tgtc 24

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
gcctgctgtg gtcacaggtc tccg 24

<210> 17  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18  
<211> 1901  
<212> DNA  
<213> Homo sapiens

<400> 18  
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50  
gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100  
ctctgcccc tgcctcctgt gcagctgctg ccccgccagc cgcaactcca 150



ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200  
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250  
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300  
tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350  
gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400  
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450  
ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct 500  
gacggctcct tcaccaacat ctggttctac ttcggcgctcg tgggctcctt 550  
cctcttcata ctcatccagc tgggtgctgt catcgacttt gcgcactcct 600  
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650  
tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700  
ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750  
agggcaaggt cttcatcagc ctcaacctca ctttctgtgt ctgcgtgtcc 800  
atcgctgctg tcctgccccaa ggtccaggac gccagccca actcgggtct 850  
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900  
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950  
ctgggcaacg agacagttgt ggcaggcccc gagggctatg agaccagtg 1000  
gtgggatgcc ccgagcattg tgggcctcat catcttcttc ctgtgcaccc 1050  
tcttcatcag tctgcgtcc tcagaccacc ggcaggtgaa cagcctgatg 1100  
cagaccgagg agtgcaccac tatgctagac gccacacagc agcagcagca 1150  
gcagggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200  
tcacctacag ctactccttc ttccacttct gcctggtgct ggcctcactg 1250  
cacgtcatga tgacgctcac caactggtac aagcccggtg agaccggaa 1300  
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
cagggtgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400  
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tgggtgcctcc 1450  
tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500  
caccaatcag ccaggctgag cccccacccc tgccccagct ccaggacctg 1550  
cccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat 1600

caggctcctg cagagcccca tccccccgcc acaccacac ggtggagctg 1650  
 cctcttcctt cccctcctcc ctgttgccca tactcagcat ctcggatgaa 1700  
 agggctccct tgtctcagg ctccacggga gcggggctgc tggagagagc 1750  
 ggggaactcc caccacagt gggcatccgg cactgaagcc ctggtgttcc 1800  
 tggtcacgtc cccagggga ccctgcccc ttctggact tcgtgcctta 1850  
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900  
 a 1901

<210> 19  
 <211> 457  
 <212> PRT  
 <213> Homo sapiens

<400> 19  
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser  
     1                    5                    10                    15  
 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro  
                     20                    25                    30  
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe  
                     35                    40                    45  
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly  
                     50                    55                    60  
 Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly  
                     65                    70                    75  
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser  
                     80                    85                    90  
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala  
                     95                    100                    105  
 Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser  
                     110                    115                    120  
 Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe  
                     125                    130                    135  
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr  
                     140                    145                    150  
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val  
                     155                    160                    165  
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile  
                     170                    175                    180

Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu		185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr		200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe		215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe		230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala		245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu		260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser		275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro		290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr		305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile		320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His		335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met		350	355	360
Leu	Asp	Ala	Thr	Gln	Gln	Gln	Gln	Gln	Gln	Val	Ala	Ala	Cys	Glu		365	370	375
Gly	Arg	Ala	Phe	Asp	Asn	Glu	Gln	Asp	Gly	Val	Thr	Tyr	Ser	Tyr		380	385	390
Ser	Phe	Phe	His	Phe	Cys	Leu	Val	Leu	Ala	Ser	Leu	His	Val	Met		395	400	405
Met	Thr	Leu	Thr	Asn	Trp	Tyr	Lys	Pro	Gly	Glu	Thr	Arg	Lys	Met		410	415	420
Ile	Ser	Thr	Trp	Thr	Ala	Val	Trp	Val	Lys	Ile	Cys	Ala	Ser	Trp		425	430	435
Ala	Gly	Leu	Leu	Leu	Tyr	Leu	Trp	Thr	Leu	Val	Ala	Pro	Leu	Leu		440	445	450
Leu	Arg	Asn	Arg	Asp	Phe	Ser										455		

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
gccgcctcat cttcacgttc ttcc 24

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 21  
tcatccagct ggtgctgctc 20

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 22  
cttcttcac ttctgcctgg 20

<210> 23  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 23  
cctgggcaaa aatgcaac 18

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 24  
caggaatgta gaaggcacc acgg 24

<210> 25  
<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

tggcacagat cttcacccac acgg 24

<210> 26

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27

<211> 1351

<212> DNA

<213> Homo sapiens

<400> 27

gagcgaggcc ggggactgaa ggtgtgggtg tgcagccctc tggcagaggg 50  
ttaacctggg tcaaatgcac ggattctcac ctctgacagt tacgctctcc 100  
cgcggcacgt ccgcgaggac ttgaagtcc tgcgcgtcaa gtttgtccgt 150  
aggctcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200  
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250  
actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300  
cccagagccc tattaccgga aatctggatg ggaccgcctc cgggagctgt 350  
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400  
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550  
cgaggcttca ttcgttatgg ctggcgctgg ggttgagaga ctgcagtgtt 600  
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650  
aagatgcctt aagccatttt gtaattgcag gagctgtcac ggggaagtctt 700  
tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750  
agccttgctg ggcaactcct taggaggcct gctgatggca tttcagaagt 800

acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850  
 catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900  
 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950  
 atgctaagaa aattgaagca ctgctaaacc ttctagaaa cccttcagta 1000  
 atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050  
 gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100  
 tctttggtca gcctgctgac aaatttaagt gctggtacct gtggtggcag 1150  
 tggtttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200  
 gtactctcac ttacttatc cttaaattta aatacatact tatgtttgta 1250  
 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350  
 t 1351

<210> 28  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala  
 1 5 10 15  
 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
 20 25 30  
 Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val  
 35 40 45  
 Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu  
 50 55 60  
 Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala  
 65 70 75  
 Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val  
 80 85 90  
 Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile  
 95 100 105  
 Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val  
 110 115 120  
 Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly  
 125 130 135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50  
 ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100  
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
 ttcgttcattg gctggcgccg aacc 324

<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> unsure  
<222> 262, 330, 371  
<223> unknown base

<400> 30  
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50  
accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100  
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200  
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
agagccaggc agaaatttat nataacc 377

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 31  
tcgtacagtt acgctctccc 20

<210> 32  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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ccaccacagt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100  
gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150  
tgccggcaac cacaggttcc aagatggttt gcgggggcctt cgcgtgttcc 200  
aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250  
gctaattgga attgctgcgt ggggcattgg ctccgggctg atttccagtc 300  
tccgagtggc cggcgtggtc attgcagtgg gcatcttctt gttcctgatt 350  
gcttttagtg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400  
tttttatatg attattctgt tacttgtatt tattgttcag ttttctgtat 450  
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500  
gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550  
aaactgctgt gggttccgaa gtgttaaccc aatgacacc tgtctggcta 600  
gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650  
gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700  
cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750  
agaaagaccc ccgcgcgaat cctagtgcac tcctttgatg agaaaacaag 800  
gaagatttcc tttcgtatta tgatcttggt cactttctgt aattttctgt 850  
taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900  
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cctttcttag catttttacc tgcaaaaaa ctttgtatgg taccactgtg 1100

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 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200  
 taaaatcaga aagtatgaga tctgtttatg ttaagggaaa tccaaattcc 1250  
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 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350  
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 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700  
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750  
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800  
 taaaagaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

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1				5					10					15

Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25					30

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35					40					45

Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50					55					60

Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65					70					75

Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80					85					90

Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95					100					105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	
				110					115					120	
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	
				125					130					135	
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	
				140					145					150	
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	
				155					160					165	
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	
				170					175					180	
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	
				185					190					195	
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							
				200											

<210> 37  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
 <223> unknown base

<400> 37  
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 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100  
 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tgggttggaaac 150  
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300  
 gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350  
 gatcctgggt gtttggtgta cctacagata caggaaccag 390

<210> 38  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 27

<223> unknown base

<400> 38

aatcccaaat tccccaat ttttggnctt ttttagggaaa gatgtgttgt 50  
ggtaaaaagt gttagtataa aaatgataat ttacttgtag tcttttatga 100  
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttta 150  
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200  
tctaattgtat aataacat t acccttcagcc tcccatcaga atggaacgag 250  
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300  
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400  
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450  
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500  
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550  
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgttttagc ccctgaaacc aggagcaaca gggnnacgct tcctggaggt 100  
tggttggtgcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200  
tggctngctg tggttaaaagt gaccactcgt gctcgccatg tgctccaatc 250  
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40  
accacgtct gcgttgctgc c 21

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 41  
gagaatatgc tggagagg 18

<210> 42  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 42  
aggaatgcac taggattcgc gcgg 24

<210> 43  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 43  
ggccccaaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44  
<211> 2061  
<212> DNA  
<213> Homo sapiens

<400> 44  
cagtcaccat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50  
tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100  
gacgctgcag tgtgaggagc ctgtctgcac tgaggagagc agctgccaca 150  
cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200  
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250  
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300  
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400  
cgtggtacaa aaggcagaca gcgggcacta ccactgcagt ggcattcttc 450  
agagccctgg tcctgggatc ccagaaacag catctgttgt ggctatcaca 500  
gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550  
acccaagca ggaagcccca tgaccctgag ttgtcagaca aagttgcccc 600  
tgcagaggtc agctgcccgc ctctcttct ccttctacaa ggatggaagg 650  
atagtgcaaa gcagggggct ctctcagaa ttccagatcc ccacagcttc 700  
agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750  
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agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300  
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ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850  
 cagagccctc atgattagga ttagtgcctt tatttaaaaa ggccccagag 1900  
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950  
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccctt 2000  
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050  
 ttgtagccta a 2061

<210> 45  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser  
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe  
 20 25 30  
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150  
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val  
 155 160 165  
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala  
 170 175 180  
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys  
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttccagcgc caattctc 18

<210> 48



<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggtt gtcctcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
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ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100  
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150  
gcacctaaac gtggacactt atggccgtcc catcctggaa gtgccagaga 200  
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ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350  
agcaggcaaa gtaccagggc cgcctgcatg tgagccacaa ggttccagga 400  
gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450  
cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500

ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550  
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ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950  
caggaaagag cctgcctgtc ttgccatca tctcatcat ctcttgtgc 1000  
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tctaaatacc agaggggaaga tgcccatagc actaggactt ggtcatcatg 1950  
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 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050  
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100  
 agggttcagt tctgctctc cactataagt ctaatgttct gactctctcc 2150  
 tgggtgctcaa taaatatcta atcataacag c 2181

<210> 52  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val  
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr  
 20 25 30  
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
 35 40 45  
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
 50 55 60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
 65 70 75  
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
 80 85 90  
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
 95 100 105  
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
 110 115 120  
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
 125 130 135  
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
 140 145 150  
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
 155 160 165  
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
 170 175 180  
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
 185 190 195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe
				200					205					210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile
				215					220					225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys
				230					235					240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser
				245					250					255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr
				260					265					270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe
				275					280					285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr
				290					295					300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His
				305					310					315
Val	Tyr	Glu	Ala	Ala	Arg									
				320										

<210> 53  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 53  
 tatccctcca attgagcacc ctgg 24

<210> 54  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 54  
 gtcggaagac atcccaacaa g 21

<210> 55  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

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<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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agcaactgag cggggaagcg cccgcgtccg gggatcggga tgtccctcct 200

ccttctcctc ttgctagttt cctactatgt tggaaacctg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaacaaaa aagtgggtgat cacttactcc agtcgtcatg 400

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<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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				20					25					30

Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45

Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
				50					55					60

Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
				65					70					75

Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
				80					85					90

Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105

Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120

Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125					130					135

Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
				140					145					150

Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
				155					160					165

Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	170		175		180
Pro Lys Ser Arg	Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu			
	185	190			195
Gln Asn Leu Thr	Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala			
	200	205			210
Gly Asn Glu Ala	Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val			
	215	220			225
Gln Tyr Val Gln	Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly			
	230	235			240
Ile Val Ala Gly	Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu			
	245	250			255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro			
	260	265			270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val			
	275	280			285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly			
	290	295			300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln			
	305	310			315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr			
	320	325			330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro			
	335	340			345
Lys Lys Val His	His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro			
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val
				575					580					585
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe
				590					595					600
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile
				605					610					615
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
				620					625					630
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
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<210> 66  
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<400> 66  
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<210> 67  
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<210> 68  
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 <213> Homo sapiens

<400> 68

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 taatctagga atgactcgtt taaggcctat tttcatgatt tctttgtagc 2300  
 atttggtgct tgacgtatta ttgtcctttg attccaaata atatgtttcc 2350  
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<210> 69  
 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
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 35 40 45  
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile



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Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly		
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Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala		
80	85	90
Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr		
95	100	105
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe		
110	115	120
Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly		
125	130	135
His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr		
140	145	150
Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe		
155	160	165
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys		
170	175	180
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala		
185	190	195
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg		
200	205	210
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu		
215	220	225
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His		
230	235	240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala		
245	250	255
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile		
260	265	270
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His		
275	280	285
Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg		
290	295	300
Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr		
305	310	315
Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu		
320	325	330
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala		

335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro	Val Leu Asn His Ala Ala	
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys	Asn His Arg Asp Val Tyr	
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu Thr	
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu Val	
395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu	Val Gly Ala Thr Ser Phe	
410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys	Pro Gly Val Tyr Thr Arg	
425	430	435
Val Thr Ser Phe Leu Asp Trp Ile His	Glu Gln Met Glu Arg Asp	
440	445	450

Leu Lys Thr

<210> 70  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 70  
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<210> 71  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 71  
 tacacgtccc tgtggttgca gatc 24

<210> 72  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 72

cggtcaatgc agaaatgac cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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 caacccttca tttaacaagt aagaatgtta aaaagtgaaa acaatgtaag 3250  
 agcctaactc catccccgt ggccattact gcataaaata gagtgcattt 3300  
 gaaat 3305

<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly	20	25	30	
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	35	40	45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	50	55	60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	65	70	75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	80	85	90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	95	100	105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly	110	115	120	

His Val Arg Gly Tyr Ser Asp Ser Ala	Val Ser Leu Ser Thr Cys
125	130 135
Ser Gly Leu Arg Gly Leu Ile Val Phe	Glu Asn Glu Ser Tyr Val
140	145 150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe	Pro
155	160 165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His	His
170	175 180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro	Ser
185	190 195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala	Thr
200	205 210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe	Gln
215	220 225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile	Glu
230	235 240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile	Arg
245	250 255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys	Cys
260	265 270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu	Asp
275	280 285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn	Ala
290	295 300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly	Met
305	310 315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly	Ile
320	325 330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr	Leu
335	340 345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr	Leu
350	355 360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly	Cys
365	370 375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe	Ser
380	385 390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly	Met
395	400 405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln  
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro  
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile  
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctaccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150  
ttgagntttt tgntaaaaca tggacatgnt tcagtgtctgc tcntgagaga 200  
gtagcagggt accacttttg gcaggcccca gccctgcagc aaggaggaag 250  
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agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350  
gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400  
ttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450  
gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggt ctcagg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 77  
catgagcatg tgcacggc 18

<210> 78  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 78  
tacctgcacg atgggcac 18

<210> 79  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 79  
cactgggcac ctcccttc 18

<210> 80  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 80  
ctccaggctg gtctccaagt ccttcc 26

<210> 81  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 81  
tccctgttgg actctgcagc ttcc 24

<210> 82  
<211> 19  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 82

cttcgctggg aagagtttg 19

<210> 83

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 83

gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84

<211> 1714

<212> DNA

<213> Homo sapiens

<400> 84

catcctgcaa catggtgaaa ccacgcctgg ctaattttgt tgtatttttg 50  
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atgatctgcc cgcctcggcc tcccaaagtg ctgggattac aggcgagtgc 150  
aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200  
tacattttta atgacaggaa aatgctcaca ataattgtta acccaaaatt 250  
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 gaatagcgtg aactcaggag gcggagcttg cagtggagccg agattgcgct 1650  
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 aaaaaaaaaa aaaa 1714

<210> 85  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<400> 85  
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 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
 35 40 45  
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu  
 50 55 60  
 Ala Leu Leu His Leu Tyr His  
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<210> 86  
 <211> 23

<212> DNA  
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<220>  
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<400> 86  
acgggcacac tggatcccaa atg 23

<210> 87  
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<212> DNA  
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<400> 87  
ggtagagatg tagaaggga agcaagacc 29

<210> 88  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 88  
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<210> 89  
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<212> DNA  
<213> Homo sapiens

<400> 89  
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gctgctgctg ggccatggcg gcggcggcg ctggggcgcc cgggcccagg 150  
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<210> 90  
 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
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 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala  
 35 40 45

Ala Asp Gly Pro	Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro	50	55	60
His Ser Lys His	Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile	65	70	75
Gln Ser Ala Ala	His Phe Val Met Phe Phe Ala Pro Trp Cys Gly	80	85	90
His Cys Gln Arg	Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys	95	100	105
Tyr Asn Ser Met	Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp	110	115	120
Cys Thr Ala His	Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly	125	130	135
Tyr Pro Thr Leu	Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys	140	145	150
Tyr Gln Gly Pro	Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu	155	160	165
Gln Thr Leu Asn	Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu	170	175	180
Pro Pro Ser Ala	Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser	185	190	195
Ala Ser Asn Phe	Glu Leu His Val Ala Gln Gly Asp His Phe Ile	200	205	210
Lys Phe Phe Ala	Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro	215	220	225
Thr Trp Glu Gln	Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val	230	235	240
Lys Ile Gly Lys	Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser	245	250	255
Gly Asn Gln Val	Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp	260	265	270
Gly Lys Lys Val	Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser	275	280	285
Leu Arg Glu Tyr	Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly	290	295	300
Ala Thr Glu Thr	Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala	305	310	315
Glu Pro Glu Ala	Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn	320	325	330

Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

<210> 91  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 91  
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<210> 92  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 92  
 ccaagccaac acactctaca g 21

<210> 93  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 93  
 aagtggtcgc cttgtgcaac gtgc 24

<210> 94  
 <211> 23



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaaggg gatatatcgc cac 23

<210> 95  
<211> 49  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

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<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150  
atttcaccag gacccaaagg agatgatggg gaaaaaggag atccaggaga 200  
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 cagttattgt tatccatcct ttttttctg attgtactac atttgatctg 950  
 agtcaacata gctagaaaat gctaaactga ggtatggagc ctccatcatc 1000  
 aaaaaaaaaa aaaaaa 1016

<210> 97  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 97

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Asp	Ser	Arg	Pro	Thr	Ala	Glu	Val	Cys	Ala	Thr	His	Thr	Ile	Ser	35	40	45	
Pro	Gly	Pro	Lys	Gly	Asp	Asp	Gly	Glu	Lys	Gly	Asp	Pro	Gly	Glu	50	55	60	
Glu	Gly	Lys	His	Gly	Lys	Val	Gly	Arg	Met	Gly	Pro	Lys	Gly	Ile	65	70	75	
Lys	Gly	Glu	Leu	Gly	Asp	Met	Gly	Asp	Gln	Gly	Asn	Ile	Gly	Lys	80	85	90	
Thr	Gly	Pro	Ile	Gly	Lys	Lys	Gly	Asp	Lys	Gly	Glu	Lys	Gly	Leu	95	100	105	
Leu	Gly	Ile	Pro	Gly	Glu	Lys	Gly	Lys	Ala	Gly	Thr	Val	Cys	Asp	110	115	120	
Cys	Gly	Arg	Tyr	Arg	Lys	Phe	Val	Gly	Gln	Leu	Asp	Ile	Ser	Ile	125	130	135	
Ala	Arg	Leu	Lys	Thr	Ser	Met	Lys	Phe	Val	Lys	Asn	Val	Ile	Ala	140	145	150	
Gly	Ile	Arg	Glu	Thr	Glu	Glu	Lys	Phe	Tyr	Tyr	Ile	Val	Gln	Glu	155	160	165	
Glu	Lys	Asn	Tyr	Arg	Glu	Ser	Leu	Thr	His	Cys	Arg	Ile	Arg	Gly	170	175	180	
Gly	Met	Leu	Ala	Met	Pro	Lys	Asp	Glu	Ala	Ala	Asn	Thr	Leu	Ile	185	190	195	
Ala	Asp	Tyr	Val	Ala	Lys	Ser	Gly	Phe	Phe	Arg	Val	Phe	Ile	Gly				

200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn		
215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser		
230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly		
245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys		
260	265	270
Glu Phe Ile Lys Lys Lys Lys		
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<210> 98  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 98  
 cgctgactat gttgccaaga gtgg 24

<210> 99  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 99  
 gatgatggag gctccatacc tcag 24

<210> 100  
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<220>  
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<210> 101  
 <211> 2574  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
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<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

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				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys	320	325	330
Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala	335	340	345
Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln	350	355	360
Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro	365	370	375
Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met	380	385	390
Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly	395	400	405
Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln	410	415	420
Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser	425	430	435
Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly	440	445	450
Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro	455	460	465
Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala	470	475	480
Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser	485	490	495
Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp	500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met	515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser	530	535	540
Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala	545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe	560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu	575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu	590	595	600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp	605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His	620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His	635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu	650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu	665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn	680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu	695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr	710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile	725	730	

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 <212> DNA  
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<220>  
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<210> 104  
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 <212> DNA  
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<220>  
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<400> 104  
 ggagaatgtg gccacaac 18

<210> 105  
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<400> 105

gccctggcac agtgactcca tagacg 26

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

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<400> 107

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<210> 108

<211> 2579

<212> DNA

<213> Homo sapiens

<400> 108

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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys  
 50 55 60  
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu  
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 80 85 90  
 Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe  
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 Asp Glu Phe Phe Arg Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu  
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Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp  
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Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg  
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<210> 114

<211> 515

<212> PRT

<213> Homo sapiens

<400> 114

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Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser	35	40	45	
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala	50	55	60	
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln	65	70	75	
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp	80	85	90	
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys	95	100	105	
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	110	115	120	
Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln	125	130	135	
Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro	140	145	150	

Asn Cys Leu Pro Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	155	160	165
Glu Val Gly Tyr Ser Thr His Met Val	Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln	425	430	435

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 Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly  
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 Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe  
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 515

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<400> 116  
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<210> 117  
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<210> 118

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<212> DNA

<213> Homo sapiens

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<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

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 gtttcaggct tatgtccaga tagcctttta tctgtggatg actgaatgtt 1800  
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 tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950  
 caatatttgc tttaaataatc atatcactgt atcttctcag tcatttctga 2000  
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 cctcngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100  
 catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150  
 ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200  
 aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250  
 gtaataataa 2260

<210> 119  
 <211> 338  
 <212> PRT  
 <213> Homo sapiens

<400> 119  
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Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly	20	25	30
Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr	35	40	45
Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val	50	55	60
Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val	65	70	75
Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr	80	85	90
Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys	95	100	105
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys	110	115	120
Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser	125	130	135
Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr	140	145	150
Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu	155	160	165
Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser	170	175	180
Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe	185	190	195
Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr	200	205	210
Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met	215	220	225
Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln	230	235	240
Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly	245	250	255
Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu	260	265	270
Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala	275	280	285
His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr	290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro  
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly  
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys  
335

<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gggagctgct gctgtggctg ctggtgctgt gcgcgctgct cctgctcttg 50

gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggttg 150

tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200

ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250

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 aagatatact tgttttgccc cttgacctga ccgacactgg ttcccatgaa 350  
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 gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
			20					25					30	

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
			35					40					45	

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
			50					55					60	



Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val  
 65 70 75  
 Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly  
 80 85 90  
 Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr  
 95 100 105  
 Arg Lys Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr  
 110 115 120  
 Lys Cys Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile  
 125 130 135  
 Val Thr Val Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser  
 140 145 150  
 Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn  
 155 160 165  
 Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser  
 170 175 180  
 Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu Asn Ser  
 185 190 195  
 Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asp Gln  
 200 205 210  
 Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile  
 215 220 225  
 Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro  
 230 235 240  
 Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala  
 245 250 255  
 Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe  
 260 265 270  
 Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys  
 275 280 285  
 Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgccc agaag 46

<210> 131  
<211> 2365  
<212> DNA  
<213> Homo sapiens

<400> 131  
gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50  
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caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150  
tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200  
tccttggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250  
cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300  
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 tttctttttt tggggggcag cagttttcct ttttttaaac ttaaataaat 2350  
 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
			20						25					30

Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe  
 35 40 45  
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn  
 50 55 60  
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln  
 65 70 75  
 Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val  
 80 85 90  
 Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu  
 95 100 105  
 Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu  
 110 115 120  
 Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro  
 125 130 135  
 Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu  
 140 145 150  
 Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln  
 155 160 165  
 Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly  
 170 175 180  
 Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu  
 185 190 195  
 Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn  
 200 205 210  
 Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met  
 215 220 225  
 Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly  
 230 235 240  
 Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp  
 245 250 255  
 Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu  
 260 265 270  
 Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp  
 275 280 285  
 Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro  
 290 295 300  
 Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly  
 305 310 315

Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp  
 320 325 330  
 Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly  
 335 340 345  
 Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys  
 350 355 360  
 Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly  
 365 370 375  
 Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly  
 380 385 390  
 Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu  
 395 400 405  
 Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys  
 410 415 420  
 Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg Gly Trp  
 425 430 435  
 Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln  
 440 445 450  
 Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu  
 455 460 465  
 His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met  
 470 475 480  
 Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu  
 485 490 495  
 Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu  
 500 505 510  
 Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg  
 515 520 525  
 Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser  
 530 535 540  
 Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu  
 545 550 555  
 Ala Glu Pro Gly Ser Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser  
 560 565 570  
 Cys

<210> 133  
 <211> 24  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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			20						25					30	
Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	
				35					40					45	
Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	
			50						55					60	
Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	
			65						70					75	
Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	
			80						85					90	
Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	
			95						100					105	
Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	
			110						115					120	
Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	
			125						130					135	
Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	
			140						145					150	
Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	
			155						160					165	
Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	
			170						175					180	
Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	
			185						190					195	
Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	
			200						205					210	
Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	
			215						220					225	

Val Leu Gln Gln Asp Ala His Xaa Ser Val Thr Ile Thr Gly Gln  
230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu  
245 250 255

Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys  
260 265 270

Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala  
275 280 285

Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln  
290 295 300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile  
305 310 315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 141  
tgccaaccag gcagctgtaa gtgc 24

<210> 142  
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<212> DNA  
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<223> Synthetic oligonucleotide probe

<400> 142  
tggaagaaga gggtggtgat gtgg 24

<210> 143  
<211> 45  
<212> DNA  
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<223> Synthetic oligonucleotide probe

<400> 143  
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<210> 144  
<211> 2336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
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<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly	35	40	45	
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly	50	55	60	
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile	65	70	75	
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln	80	85	90	
Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile	95	100	105	
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro	110	115	120	
Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg	125	130	135	
Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn	140	145	150	

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
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Leu

<210> 146  
 <211> 26  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 147  
 <211> 25  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 147  
 gcccagagca ggaggaatga tgagc 25

<210> 148  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 149  
 <211> 2196  
 <212> DNA  
 <213> Homo sapiens

<400> 149  
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caccctctcc cgtagccac ccgactaaca tctcagtctc tgaaaatgca 150  
cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200  
tctttttctc tttggtgcc aaggacgga gcatggaggt cacagtacct 250  
gccaccctca acgtcctcaa tggctctgac gcccgcctgc cctgcacctt 300  
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350  
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aagatcatta acctgaagct ggagcggttt caagaccgcg tggagttctc 450  
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<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

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				20					25					30

Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45

Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60

Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75

Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90

Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105

Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



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125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 103, 233  
 <223> unknown base

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 ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
 gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcca 200  
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250  
 aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300  
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350  
 ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400  
 tggagcgggt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450  
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 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
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cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250  
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tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350  
ctacatcatg aaccccc 368

<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
gcacgtttct cagcatcacc gac 23

<210> 155  
<211> 50  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 155

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<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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cgcggaacca gcgtcccg cgggacgtca cccccagtgt gtgtgtgtcc 150  
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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

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Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly	
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Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val	
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Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile	
				65					70					75	
Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp	
				80					85					90	
Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr	
				95					100					105	
Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys	
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Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly	
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Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr	
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Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg	
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Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met	
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Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val	
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Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg	
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Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser	
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Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu	
				230					235					240	
Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys	

245										250					255				
Ile	Arg	Glu	Gln	Gln	Arg	Ser	Ala	Val	Ser	Thr	Ser	Trp	Leu	Leu					
				260					265					270					
Pro	Tyr	Asn	Tyr	Thr	Trp	Ser	Pro	Glu	Lys	Val	Phe	Val	Gln	Thr					
				275					280					285					
Pro	Thr	Ile	Asn	Tyr	Thr	Leu	Arg	Asp	Tyr	Arg	Lys	Phe	Phe	Gln					
				290					295					300					
Asp	Ile	Gly	Phe	Glu	Asp	Gly	Trp	Leu	Met	Arg	Gln	Asp	Thr	Glu					
				305					310					315					
Gly	Leu	Val	Glu	Ala	Thr	Met	Pro	Pro	Gly	Val	Gln	Leu	His	Cys					
				320					325					330					
Leu	Tyr	Gly	Thr	Gly	Val	Pro	Thr	Pro	Asp	Ser	Phe	Tyr	Tyr	Glu					
				335					340					345					
Ser	Phe	Pro	Asp	Arg	Asp	Pro	Lys	Ile	Cys	Phe	Gly	Asp	Gly	Asp					
				350					355					360					
Gly	Thr	Val	Asn	Leu	Lys	Ser	Ala	Leu	Gln	Cys	Gln	Ala	Trp	Gln					
				365					370					375					
Ser	Arg	Gln	Glu	His	Gln	Val	Leu	Leu	Gln	Glu	Leu	Pro	Gly	Ser					
				380					385					390					
Glu	His	Ile	Glu	Met	Leu	Ala	Asn	Ala	Thr	Thr	Leu	Ala	Tyr	Leu					
				395					400					405					
Lys	Arg	Val	Leu	Leu	Gly	Pro													
				410															

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
gccccaaatg aaaacgggcc ctacttcctg gccctccgag agatg 45

<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150  
tcttcgcctt gatcgtgttc tcttcgcatc atggtgaggg ctacagcaat 200  
gccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250  
ctgccgctat ggcagtgcca tcgggggtgt ggccttcctg gcctcggcct 300  
tcttcttggt ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350  
cgcaagtacc tgggtcattg tgacctgtc ttctcagctc tctggacctt 400  
cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450  
accgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500  
ttcagcttct tttccatctt ctctgggggt gtgctggcct ccctggccta 550  
ccagcgctac aaggctggcg tggacgactt catccagaat tacgttgacc 600  
ccactccgga cccaacact gcctacgcct cctaccaggg tgcattctgtg 650  
gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700  
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cagagagggc cctccctct gccctggact ttccatcag cctcctggaa 800  
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ccgcctgcag tggctagaag ccagcaggtg cccatgtgct actgacaagt 1050  
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 gcgttctctg ccaaagactc gtgggggcca tcacacctgc cctgtgcagc 1150  
 ggagccggac caggctcttg tgtcctcact caggtttgct tcccctgtgc 1200  
 ccactgctgt atgatctggg ggccaccacc ctgtgccggt ggcctctggg 1250  
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 tgctcccacc cctggcagca ggggaagggt ttgcctgaca acaccagct 1350  
 ttatgtaaat attctgcagt tgttacttag gaagcctggg gagggcaggg 1400  
 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450  
 tgggggagat gcccggcctg ggatgctgtt tggagacgga ataaatgttt 1500  
 tctcattcaa ag 1512

<210> 162  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 162

Met	Glu	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe	1	5	10	15
Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala	20	25	30	
Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150	



Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu  
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn  
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr  
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln  
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr  
215 220

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcgggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaagggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166

ccaggaggct catgggaaaag tcc 23

<210> 167

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

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agggtgatca gtgagcagaa ggatgcccggt ggccgaggcc cccaggtgg 100  
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150  
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200  
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250  
gggtgctact ctggtatttc ctagggtaca aggcggaggt gatggtcagc 300  
caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350  
tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400  
agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450  
aactccagct ccgtctattc ctttggggag ggaccctca cctgcttctt 500  
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tgggttggtta ccgctacagc tacgtgggccc agggccagggt cctccggctg 750  
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caaggacctc atgctcaaac tccggctgga gtggacgctg gcagagtgcc 850  
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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp
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Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala
			20						25				30	

Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val
			35						40				45	

Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly
			50						55				60	

Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val
			65						70				75	

Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe
			80						85				90	

Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

95	100	105
Thr Ala Lys Ala Gln Lys Met Leu Lys	Glu Leu Ile Thr Ser Thr	
110	115	120
Arg Leu Gly Thr Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe Gly	
125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile Pro	
140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro	Glu Val Val Gln Ala Leu	
155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala Val	
170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp	Pro Glu Gly Leu Val Ile	
185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr Leu	
200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu Arg	
215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser	Ser Cys Leu Trp His Leu	
230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp Thr	
245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala Gly	
260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser Arg	
275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala	Ser Gly Ala Ile Met Ala	
290	295	300
Val Val Trp Lys Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe Val	
305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln	Ala Cys Glu Val Asn Leu	
320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr Pro	
335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp His	
350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe Asp	
365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr Gln	

380	385	390
Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile 395 400 405		
Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly 410 415 420		
Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly 425 430 435		
Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro 440 445 450		
Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys 455 460 465		
Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys 470 475 480		
Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile 485 490 495		
Ser Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly 500 505 510		
Ser Asp Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe 515 520 525		
Thr Phe Gln Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro 530 535 540		
Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu 545 550 555		
His Cys Asp Cys Gly Leu Gln Gly Pro Ser Ser Arg Ile Val Gly 560 565 570		
Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu 575 580 585		
Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp 590 595 600		
Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met 605 610 615		
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln 620 625 630		
Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu 635 640 645		
Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val 650 655 660		
Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val		

665					670					675				
Arg	Pro	Val	Cys	Leu	Pro	Ala	Arg	Ser	His	Phe	Phe	Glu	Pro	Gly
				680					685					690
Leu	His	Cys	Trp	Ile	Thr	Gly	Trp	Gly	Ala	Leu	Arg	Glu	Gly	Gly
				695					700					705
Pro	Ile	Ser	Asn	Ala	Leu	Gln	Lys	Val	Asp	Val	Gln	Leu	Ile	Pro
				710					715					720
Gln	Asp	Leu	Cys	Ser	Glu	Ala	Tyr	Arg	Tyr	Gln	Val	Thr	Pro	Arg
				725					730					735
Met	Leu	Cys	Ala	Gly	Tyr	Arg	Lys	Gly	Lys	Lys	Asp	Ala	Cys	Gln
				740					745					750
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Lys	Ala	Leu	Ser	Gly	Arg
				755					760					765
Trp	Phe	Leu	Ala	Gly	Leu	Val	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Arg
				770					775					780
Pro	Asn	Tyr	Phe	Gly	Val	Tyr	Thr	Arg	Ile	Thr	Gly	Val	Ile	Ser
				785					790					795
Trp	Ile	Gln	Gln	Val	Val	Thr								
				800										

<210> 170  
 <211> 1327  
 <212> DNA  
 <213> Homo sapiens

<400> 170  
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 caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150  
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200  
 tgtttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
 cccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300  
 gcaaagagga cagcacatgc atctcactgc ccaagggtctg tgatgggcag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450  
 ccaaccgcga gtgtgatggg cggcccgaact gcagggacgg ctcgatgag 500  
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 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcattgctgt 1050  
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100  
 ggtccgctgg tgtgcaaggc actcagtggc cgctgggttc tggcggggct 1150  
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 cccgcatac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250  
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<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccactgcttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

atggcctcca cggctgtgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

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<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

aggcaggac acagagtcca ttcac 25

<210> 176

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

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ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ccttctctgc 100

ctccagtccc ccagcccctg gccgagagaa ggtcttacc ggccgggatt 150

gctggaaaca ccaagagggt gtttttgttt tttaaaactt ctgtttcttg 200

ggaggggggtg tggcggggca ggatgagcaa ctccgttccct ctgctctgtt 250

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ccagaggggac ggctggaaga taagctccac aaacccaaag ctacacagac 350  
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aaaaaaaaaa 1510

<210> 178  
<211> 354  
<212> PRT  
<213> Homo sapiens

<400> 178

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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser  
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg  
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg  
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg  
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro  
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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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acgcgctgga ggagtggagc agcaccggc cggccctggg ggctgacagt 150  
cggcaaagtt tggcccgaag aggaagtggc ctcaaaccct ggcaggtggc 200  
gaccaggcca gaccaggggc gctcgctgcc tgcgggcggg ctgtaggcga 250  
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<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1		5		10		15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp		20		25		30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro		35		40		45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu		50		55		60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys		65		70		75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro		80		85		90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu		95		100		105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly		110		115		120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln		125		130		135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His		140		145		150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys		155		160		165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro		170		175		180
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr						

185	190	195
Leu Glu Asp Phe Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr His	
200	205	210
Leu Ala Ser Val Ser His Pro Gln Ser	Cys His Trp Leu Leu Asp	
215	220	225
Pro His Asp Gly Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu Asp	
230	235	240
Leu Gly Phe Gly Asp Ala Val His Val	Tyr Asp Gly Pro Gly Pro	
245	250	255
Pro Glu Ser Ser Arg Leu Leu Arg Ser	Leu Thr His Phe Ser Asn	
260	265	270
Gly Lys Ala Val Thr Val Glu Thr Leu	Ser Gly Gln Ala Val Val	
275	280	285
Ser Tyr His Thr Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn Ala	
290	295	300
Thr Tyr His Val Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro Cys	
305	310	315
Gly Leu Gly Ser Gly Leu Gly Ala Gly	Glu Gly Leu Gly Glu Arg	
320	325	330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys Ala	
335	340	345
Asp Gly Thr Asp Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly His	
350	355	360
Phe Pro Cys Gly Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys Tyr	
365	370	375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp Gly	
380	385	390
Ala Asp Glu Arg Arg Cys Arg His Cys	Gln Pro Gly Asn Phe Arg	
395	400	405
Cys Arg Asp Glu Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp Gly	
410	415	420
Gln Pro Asp Cys Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser Tyr	
425	430	435
Val Leu Pro Arg Lys Val Ile Thr Ala	Ala Val Ile Gly Ser Leu	
440	445	450
Val Cys Gly Leu Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys Lys	
455	460	465
Leu Tyr Ala Ile Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro Leu	



470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser		
485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp		
500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu		
515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly		
530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg		
545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn		
560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser		
575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg		
590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro		
605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala		
620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro		
635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly		
650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro		
665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp		
680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu		
695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr		
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgctgtgctg tgcacaatct cag 23

<210> 188  
<211> 45  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
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gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150  
 aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
 tgcgggtggc actaactgtg acatctatga ccttttttat catcgacaaa 250  
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350  
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 agttggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500  
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550  
 cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600  
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 aaaaaaaaaaaa aaa 663

<210> 190  
 <211> 152  
 <212> PRT  
 <213> Homo sapiens

<400> 190  
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 Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val  
 20 25 30  
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr  
 35 40 45  
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile  
 50 55 60  
 Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe  
 65 70 75  
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe  
 80 85 90  
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr  
 95 100 105  
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys  
 110 115 120  
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn  
 125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
 140 145 150

Val Leu

<210> 191  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 78, 212, 234, 487  
 <223> unknown base

<400> 191  
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 ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
 catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
 ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250  
 aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
 atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
 gcctttgctt gatattatca actcactggg aacaacagta ttcattgctca 400  
 tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450  
 ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 192  
 cgttttgcag aacctactca ggcag 25

<210> 193  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

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gccgccccgg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200  
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<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
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Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
			20						25					30

Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
				35					40					45

Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
				50					55					60

Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala	65	70	75
Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg	80	85	90
Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu	95	100	105
Gln Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Ala Gly	110	115	120
Thr Pro His Ser Tyr Ile Asp Thr Tyr Phe Asp Thr Glu Arg Ser	125	130	135
Ser Thr Tyr Arg Ser Lys Gly Phe Asp Val Thr Val Lys Tyr Thr	140	145	150
Gln Gly Ser Trp Thr Gly Phe Val Gly Glu Asp Leu Val Thr Ile	155	160	165
Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn Ile Ala Thr Ile	170	175	180
Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys Trp Asn Gly	185	190	195
Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser Ser Ser	200	205	210
Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile Pro	215	220	225
Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala	230	235	240
Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu	245	250	255
Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu	260	265	270
Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly	275	280	285
Gln Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala	290	295	300
Ile Val Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val	305	310	315
Phe Asp Ala Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro	320	325	330
Glu Phe Ser Asp Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp	335	340	345

Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile  
 350 355 360  
 Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile  
 365 370 375  
 Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn  
 380 385 390  
 Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu  
 395 400 405  
 Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp  
 410 415 420  
 Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu  
 425 430 435  
 Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr  
 440 445 450  
 Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu  
 455 460 465  
 Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly  
 470 475 480  
 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg  
 485 490 495  
 Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser  
 500 505 510  
 Ser Leu Val Arg His Arg Trp Lys  
 515

<210> 197  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 197  
 cgcagaagct acagattctc g 21

<210> 198  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 198  
 ggaaattgga ggccaaagc 19



<210> 199  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 199  
ggatgtagcc agcaactgtg 20

<210> 200  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 200  
gccttggtc gttctcttc 19

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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
ggtcctgtgc ctggatgg 18

<210> 202  
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<220>  
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<400> 202  
gacaagacta cctccgttg tc 22

<210> 203  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 203  
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 204  
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
<211> 1939  
<212> DNA  
<213> Homo sapiens

<400> 205  
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 taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Gly	Ala	Tyr
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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile	80	85	90
Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe	95	100	105
Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile	110	115	120
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe	125	130	135
Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr	140	145	150
His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val	155	160	165
Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe	170	175	180
Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg	185	190	195
Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu	200	205	210
Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala	215	220	225
His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro	230	235	240
Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu	245	250	255
Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu	260	265	270
Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys	275	280	285
His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala	290	295	300
His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro	305	310	315
Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser	320	325	330
Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr	335	340	345
Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln  
365 370 375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttggacttgg ccag 24

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac gggttgacat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

<400> 210

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gctcatcatg ggaggcatgg ctgaggactc cccgccccag atcctagtcc 100

acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150

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<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met	Gly	Gly	Met	Ala	Gln	Asp	Ser	Pro	Pro	Gln	Ile	Leu	Val	His
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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
			20						25					30
Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45
Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60
Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90
Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105
Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120
Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135



Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr  
 425 430 435  
 Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala  
 440 445 450  
 Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val  
 455 460 465  
 Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly  
 470 475 480  
 Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met  
 485 490 495  
 Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr  
 500 505 510  
 Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg  
 515 520 525  
 Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu  
 530 535 540  
 Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp  
 545 550 555  
 Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser  
 560 565 570  
 Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu  
 575 580 585  
 Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp  
 590 595 600  
 Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu  
 605 610 615  
 Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln  
 620 625 630  
 His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu  
 635 640 645  
 Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser  
 650 655 660  
 Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala  
 665 670 675  
 Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg  
 680 685 690  
 His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr  
 695 700 705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser  
 710 715 720  
 Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys  
 725 730 735  
 Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro  
 740 745 750  
 Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu  
 755 760 765  
 Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu  
 770 775 780  
 Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro  
 785 790 795  
 Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser  
 800 805 810  
 Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly  
 815 820 825  
 Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro  
 830 835 840  
 Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp  
 845 850 855  
 Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu  
 860 865 870  
 Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala  
 875 880 885  
 Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu  
 890 895 900  
 Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro  
 905 910 915  
 Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro  
 920 925 930  
 Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser  
 935 940 945  
 His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp  
 950 955 960  
 Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro  
 965 970 975  
 Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser  
 980 985

<210> 212  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 212  
gaagggacct acatgtgtgt ggcc 24

<210> 213  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 213  
actgaccttc cagctgagcc acac 24

<210> 214  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 214  
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215  
<211> 2749  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1869, 1887  
<223> unknown base

<400> 215  
ctccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50  
ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100  
gcgggttcga aggggacact gtgtccctgc agtgcaccta caggaagag 150  
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200  
tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250  
agggcagggg gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350  
cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400  
caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450  
acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500  
attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550  
agacaggggc tgaggccctt ccattgccag ggacttccca gtacgggcac 600  
gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650  
tcctgcaggg agtccccgcc ccccatgca gctggactcc acctcagcag 700  
aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750  
atccccgatg tccgcatact ggccccagtc ctgggtgctg tgagccttct 800  
gtcagccgca ggccctgatc ccttctgcag ccacctgctc ctgtggagaa 850  
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tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950  
ggacgtgatc tcgatgcctc cctccacac atctgaggag gagctgggct 1000  
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cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagctttc 1100  
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tccccaggct ctctcttgc atgttccagc ctgacctaga agcgtttgc 1200  
agccctggag ccagagcgg tggccttgct cttccggctg gagactggga 1250  
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cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350  
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 acagaagtgg ttgcctttnc cttttgccct ccctggncca tgccttcttg 1900  
 cctttggaaa aatgatgaa gaaaaccttg gctccttcct tgtctggaaa 1950  
 gggttacttg cctatgggtt ctgggtggcta gagagaaaag tagaaaacca 2000  
 gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcgggatac 2050  
 ctgaaggtga ctccgagtcc agccccctgg agaaggggtc ggggggtggtg 2100  
 gtaaagtagc acaactacta ttttttttct ttttccatta ttattgtttt 2150  
 ttaagacaga atctcgtgct gctgcccagg ctggagtgca gtggcacgat 2200  
 ctgcaaactc cgcctcctgg gttcaagtga ttcttctgcc tcagcctccc 2250  
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 ctttttagtag agatgggggtt tcaccatggt ggccaggctg gtcttgaact 2350  
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 caggcatgag cactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450  
 agagttgttc agtatgcaaa acttggaag atggaggaga aaaagaaaag 2500  
 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550  
 tttgtgtac ttcttccac tcttttcttc ttcacataat ttgccggtgt 2600  
 tctttttaca gagcaattat cttgtatata caactttgta tctgccttt 2650  
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700  
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
1				5					10					15

Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
			20						25					30

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35					40					45

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Gly Gln Glu Thr Met		
65	70	75
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu		
80	85	90
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr		
95	100	105
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile		
110	115	120
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser		
125	130	135
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala		
140	145	150
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu		
155	160	165
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu		
170	175	180
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr		
185	190	195
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro		
200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala		
215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg		
230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu		
245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His		
260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln		
275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys		
290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro		
305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val		
320	325	330
Ser Ala		

<210> 217  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 217  
ccctgcagtg cacctacagg gaag 24

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 218  
ctgtcttccc ctgcttggt gtgg 24

<210> 219  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 219  
ggtgcaggaa ggggtgggac ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100  
cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150  
tggcgtgac atagctcact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250  
cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300  
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350  
ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgcca 400



gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450  
 ctccagttag gccaaagtctt acggtcggtt tgaactggcc agagtgttac 500  
 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550  
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600  
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650  
 ggtgcagcaa cctcaccctg aacgtcccca acgtgtgccg gatgtactgc 700  
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750  
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser	1	5	10	15
Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu	20	25	30	
His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp	35	40	45	
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala	50	55	60	
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln	65	70	75	
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro	80	85	90	
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu	95	100	105	
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln	110	115	120	
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys	125	130	135	
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe	140	145						

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 222  
gggatcatgt tggtggccct ggtc 24

<210> 223  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 223  
gcaaggcaga ccagtcagc cag 23

<210> 224  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 224  
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225  
<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
agccgctgcc ccgggccggg cgcccgcggc ggcacatga gtccccgctc 50  
gtgcctgcgt tcgctgcgcc tctcgtctt cgccgtcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaaagtgt cgtcgggtggg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
gatgtgcaag cggaacctgg aagtcattga ctcggtgcgc gcggtgccc 250  
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300  
tgctccacac tcgactcctt gcccgctctc ggcaaggtgg tgacgcaagg 350  
gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400  
ttgcagtgc gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500  
ctctgacaac atcgccctacg gtgtggcctt ctcacagtcg tttgtggatg 550  
tgcgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600  
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650  
atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700  
gagccgtgcc gcccttccgc cagggtgggtc acgcactgaa ggagaagttt 750  
gatggtgcca ctgagggtga gccacgccgc gtgggctcct ccagggcact 800  
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850  
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aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200  
ctggtttggt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250  
caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300  
ctgccactga ccaaaggac cttgctcgtg ccgctggctg cccgcatgtg 1350  
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gtcatcgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500  
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tacacatgga ctctggcag cttgagccta gaagccatgt ctctcaaatg 1600  
ccctgagaaa ggaacaagc agataccagg tcaagggcac caggttcatt 1650  
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gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800  
agaccacct aggcaggcat ataggctgcc atcctggacc agggatcccc 1850

gctgtgcctt tgcagtcac cccgagtcac ctttcacagc gctgttcctc 1900  
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
 ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226  
 <211> 351  
 <212> PRT  
 <213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1				5					10					15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
			20						25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
			35						40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
			50						55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
			65						70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
			80						85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
			95						100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
			110						115					120
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
			125						130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
			140						145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
			155						160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
			170						175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
			185						190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
			200						205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 227  
 gctgcagctg caaattccac tgg 23

<210> 228  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 228  
 tgggtgggaga ctgtttaaat tatcggcc 28

<210> 229  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

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gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100  
gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150  
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200  
ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250  
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gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350  
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400  
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450  
cgctgaccc agggcttggc tgaagccggc aggggccgtg aggacgtccg 500  
cactgagctg ttccggggcg tggaggccgt gaggctccag aacaactcct 550  
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tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700  
tcactcgga cgcgcgtggc cgtggttact ggctgggcct gagggtgtg 750  
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cagcttcagc cactggaacc agggagagcc caatgacgt tgggggcgcg 850  
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900  
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
ccgccagtg ccctggagcc gcgccattg cagcatgtcg tctctgggg 1000  
gctgctcacc tccctggctc ctggagctga ttgcaaaga gttttttct 1050  
tcctcatcca ccgctgctga gtctcagaaa cacttgccc aacatagccc 1100  
tgtccagccc agtgccctggg ctctgggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200  
 ctctgcgctc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250  
 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300  
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
 aaaaa 1355

<210> 231  
 <211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 231  
 Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
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 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
 20 25 30  
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
 35 40 45  
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
 50 55 60  
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
 65 70 75  
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
 80 85 90  
 Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
 95 100 105  
 Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
 110 115 120  
 Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
 125 130 135  
 Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg  
 140 145 150  
 Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys  
 155 160 165  
 Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser  
 170 175 180  
 Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp  
 185 190 195  
 Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly  
 200 205 210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu  
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val  
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro  
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr  
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp  
275 280 285

Ile Cys Glu Lys Arg His Asn Cys  
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<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens



<400> 235

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ctccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150  
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gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250  
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gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400  
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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 236

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				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val
				110					115					120
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
				125					130					135
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
				140					145					150
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
				155					160					165

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala  
 170 175 180  
 Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe  
 185 190 195  
 Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val  
 200 205 210  
 Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe  
 215 220 225  
 Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr  
 230 235 240  
 Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala  
 245 250 255  
 Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser  
 260 265 270  
 Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser  
 275 280 285  
 Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser  
 290 295 300  
 Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro  
 305 310 315  
 Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys  
 320 325 330  
 Val

<210> 237  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 237  
 cagcactgcc aggggaagag gg 22

<210> 238  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 238  
 caggactcgc tacgtccg 18

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
cagccccttc tcttcctttc tccc 24

<210> 240  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 240  
gcagttatca gggacgcact cagcc 25

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 241  
ccagcgagag gcagatag 18

<210> 242  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 242  
cggtcaccgt gtcctgcggg atg 23

<210> 243  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
cagccccttc tcttcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

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aggaagagtg tactcgtagg cggacagctt tagtgccgg ccggccgctc 150  
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300  
cagaaatddd atccaacttt gtttggaagc ttattatgac aataccattt 350  
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400  
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450  
tcattcacgg ttgcgtttta atcgagagg actggttgcc atggcaaatg 500  
ctggttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550  
gatgaactta acaataagca taccatcttt ggaaaggta caggggatac 600  
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650  
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 catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850  
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
			20					25						30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
			35					40						45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
			50					55						60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
			65					70						75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
			80					85						90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
			95					100						105
Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala
			110					115						120
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly
			125					130						135

Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp  
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg  
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met  
455 460 465

Arg Glu Lys Lys Glu Arg Arg  
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<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tggtgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250



<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
ctggttcagc agtgcaaggg tctg 24

<210> 251  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
cctctccgat taaaacgc 18

<210> 252  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 252  
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253  
<211> 2456  
<212> DNA  
<213> Homo sapiens

<400> 253  
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gatgctgccc ggccgcctc ggctttgagg cgagagaagt gtcccagacc 100  
catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150  
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<210> 254

<211> 545

<212> PRT

<213> Homo sapiens

<400> 254

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				20					25					30
Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly
				35					40					45
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser
				50					55					60
Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly
				65					70					75
Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg
				80					85					90
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met
				95					100					105
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe
				110					115					120
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro
				125					130					135

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro	140	145	150
Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg	155	160	165
Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu	170	175	180
Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu	185	190	195
Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg	200	205	210
Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val	215	220	225
Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met	230	235	240
Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser	245	250	255
Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val	260	265	270
Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp	275	280	285
Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala	290	295	300
Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp	305	310	315
Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser	320	325	330
Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His	335	340	345
Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile	350	355	360
Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala	365	370	375
Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg	380	385	390
Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg	395	400	405
Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro  
 425 430 435  
 Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu  
 440 445 450  
 Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn  
 455 460 465  
 Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp  
 470 475 480  
 Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met  
 485 490 495  
 Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr  
 500 505 510  
 Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala  
 515 520 525  
 Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu  
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 Pro Gln Glu Trp Ala  
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 <211> 23  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 255  
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<210> 256  
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<400> 256  
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<210> 257  
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 <212> DNA  
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<220>  
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<400> 257

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<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

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ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150  
tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200  
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250  
agggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300  
accgggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350  
cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400  
gggtggagag aggaagctat gtgacatata atttcatgaa cgatggggttc 450  
tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500  
caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550  
agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttgttatc 600  
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ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750  
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gcccggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850  
acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900  
ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtcctgga 950  
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aatcggcatc acggctcttc ttttctctg cctggccctg atcatcatga 1300  
agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350  
tcccggcaca gcacgatcct ggattacatc aatgtggtcc cgacggctgg 1400  
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cccctctcc accaggtgct ccctccccag aatcaaagaa gaaccagaaa 1500  
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cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600  
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tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050  
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cccagcactt tgggaggcta aggtgggtgg attgcttgag cccaggagtt 2200  
cgagaccagc ctgggcaaca tggtgaaacc ccatctctac aaaaaataca 2250  
aaacatagct gggcttggtg gtgtgtgcct gtagtcccag ctgtcagaca 2300  
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cccaaaaggg ggaggaatga ataatccacc cttgttttag caaataagca 2650

agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700

ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met	Leu	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Gly	Gly	Ser	Gln
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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25				30	
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40				45	
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55				60	
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70				75	
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85				90	
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100				105	
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115				120	
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130				135	
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145				150	
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160				165	
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175				180	
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190				195	
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205				210	
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220				225	



Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg  
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu  
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctgggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagaggggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgccca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250  
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350  
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400  
tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450  
tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500  
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550  
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600  
agcttacttc aaggccagcc atatttttct gttgaaccaa caacaggagt 650  
cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700  
taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750  
acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800  
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gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950  
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agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400  
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atttaaa 2857

<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys		20	25	30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp		35	40	45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser		50	55	60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285	

Gly Glu Asn Ala Glu Met Asp Tyr Ser	Ile Glu Glu Asp Asp Ser
290	295 300
Gln Thr Phe Asp Ile Ile Thr Asn His	Glu Thr Gln Glu Gly Ile
305	310 315
Val Ile Leu Lys Lys Lys Val Asp Phe	Glu His Gln Asn His Tyr
320	325 330
Gly Ile Arg Ala Lys Val Lys Asn His	His Val Pro Glu Gln Leu
335	340 345
Met Lys Tyr His Thr Glu Ala Ser Thr	Thr Phe Ile Lys Ile Gln
350	355 360
Val Glu Asp Val Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr Tyr
365	370 375
Val Phe Glu Val Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val Gly
380	385 390
Val Val Ser Ala Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile Arg
395	400 405
Tyr Ser Ile Thr Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn Gly
410	415 420
Thr Ile Thr Thr Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala Trp
425	430 435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu Gln
440	445 450
Ile Ser Ser Ile Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn Asp
455	460 465
His Ala Pro Glu Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys Glu
470	475 480
Asn Ala Gly Ser Gly Gln Val Ile Gln	Thr Ile Ser Ala Val Asp
485	490 495
Arg Asp Glu Ser Ile Glu Glu His His	Phe Tyr Phe Asn Leu Ser
500	505 510
Val Glu Asp Thr Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn Gln
515	520 525
Asp Asn Thr Ala Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn Leu
530	535 540
Gln Glu Glu Pro Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp Asn
545	550 555
Gly Ile Pro Ser Leu Thr Ser Thr Asn	Thr Leu Thr Ile His Val
560	565 570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln  
 575 580 585  
 Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala  
 590 595 600  
 Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr  
 605 610 615  
 Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys  
 620 625 630  
 Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly  
 635 640 645  
 Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
 650 655 660  
 Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
 665 670 675  
 Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
 680 685 690  
 Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
 695 700 705  
 Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
 710 715 720  
 Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
 725 730 735  
 Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
 740 745 750  
 Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
 755 760 765  
 Ser Ala Val Gln Ser Asn Asn  
 770

<210> 265  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 24, 60, 141, 226, 228, 249, 252  
 <223> unknown base

<400> 265  
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 gaatattttt taaaatggat agagaactgc aagatgagta ttgggtaatc 100

attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200  
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
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<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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cccgccctaa cttcctccgc ggggccagc caccttcggg agtccgggtt 150



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cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250  
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gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450  
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cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250  
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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
				125					130					135					
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr					
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<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
 tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggceacc 300  
 gttggcatga agtgtatgaa gtgcttgga gacgatgagg tgcagaagat 350  
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 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450  
 gaccctatga cccagtcaa tgccaggtag gaatttggtc aggctctctt 500  
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
 gctgttcctg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

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 cntcagcaact gccctgcccc agtggaggat ttactctat nccggcnaca 150  
 acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcttgcgtg 200  
 tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250  
 atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300  
 ctctgggag tgatagcaat cttnttgcc accgttgtnn ntgaagtga 350  
 tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
 gggggcgca tatttcttct tgcaggctctg gctatttttag ttgccacagc 450  
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
<223> unknown base

<400> 273

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gatgaancgc gccatcntca gactccctgc cccatggaga tttncctat 100  
gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcatatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atgggtggtg 250  
gcatcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttgacagg tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450  
cccagtcaat gccaggtagc aatttggtca ggctctcttc actggctggg 500  
ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550  
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

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ttaccgaggg gctttggatg tontgcntgt cgcagagcac cgggcagatc 150  
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
caaccctgac cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
ttgtggccac cgttggcatg aagtgtatga agtgcttgga agacgatgag 300  
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caggctctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
cnngnnntct atgaccctat gaccccagtc aatgccaggt acgaatttgg 450

tcaggctctc ttactggct gggctgctgc ttctctctgc cttctgggag 500

gtgccctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

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gcagcacatt ncaagcaacc ccttgcccttg aagggtggtg ncatcccccc 100

tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300

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ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<400> 276

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cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgcgtgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcattcttc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgcgatattt ctntttgcag gtctggctat tttagttgcc acagcatggg 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

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ccccagtcaa tgccaggtac gaatttgggc aggctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

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aagtctttga ctccctgctg aatctgagca gcacattgca agcaacctg 200

ccttgatggt ggttggcatc ctccctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgta tgaagtgctt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgcca tatttcttct tgcaggctctg 350

gctatttttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcactg gctgggctgc tgcttctctc tgccttctgg gaggtgccct 500

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<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
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acaacatcgt gaccnccag gccatgtacg aggggctgtg gatgtcngcg 150  
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tcaatgccag gtacgaattt ggtcaggctc tcttcaactg ctgggctgct 500  
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<210> 280  
<211> 21  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
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<210> 281  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 281  
gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
<211> 43



<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

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<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

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<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

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Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys	230	235	240
Ile Ala Leu			

<210> 285  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

gtcagtccttc tagattgtcc ttatcccacc tttcaaccan tactcacatt 50  
tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100  
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150  
cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200  
cttctagtac tagttgagag tttgactgtg aattaatttt atgccataaa 250  
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50  
gattacctcc ttaaatagaca cnttccctcg cctgttggtg ctggccttg 100  
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggcccaactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400  
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450  
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242  
<223> unknown base

<400> 287  
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cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150  
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
agttaaaaat gtatagtaac 270

<210> 288  
<211> 428  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351  
<223> unknown base

<400> 288  
ggtggcccat tcccggccca ggctgctttc cggtnntcag ttctgtccaa 50  
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200  
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250  
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300  
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400  
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289  
<211> 320  
<212> DNA  
<213> Homo sapiens

<400> 289  
tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
tactcgatcat aagtgaagagg cgtgtgttga ctgattgacc cagcgtttg 150  
gaaataaatg gcagtgcctt gttcacttaa agggaaccaag ctaaatttgt 200  
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
atttaactta tttaatgtat ttcattcat gttttcttat tgcacaaga 300  
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50  
gaaaccntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100  
ttggtagggc ttggtacatg atgctggatt acctctctta aaatgacacc 150  
cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200  
ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250  
cccaggctgc tttccgtgct ttcagttctg tccaagccat cagctccttg 300  
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacagc 400  
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500  
atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550  
acaagggtag agttaatgct gcgtgctgct gaantctgtt gggatgaantg 600  
gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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cacagtagtc cccacgtggc ccactcccgg cccaggctgc tttccgtgtc 100  
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
gagagggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250  
tgctttgttc acttaaagg accaagctaa atttgtattg gttcatgtag 300  
tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350  
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400  
gcgtgctgct gaactctgtt gggatgaactg gtattgctgc tggagggctg 450  
tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagacc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150  
gtctcacttt gttgcccagg ctggagttca gtgccatgat catgggtttac 200  
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250  
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300  
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atthttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400  
ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450  
tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500  
ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550  
cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600  
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cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750  
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aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900  
agctagtggg ggtgaccaa gagaggggtac cagagagcat ctgcaggaga 950  
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actatgtctt tctggagctg aagcgtgctc aaaaaagaa atacatggaa 1150  
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tcgggctoca ccggttcggg ggtctatctg cgtctgaaag atccagacaa 1350  
aaagaattgg aagcgcaaaa tcattgcggg ctactcaggg caccagtggg 1400



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 ctcagggtcc tactctaaga agaactaat aggatgctgg ttgtgtatta 1900  
 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950  
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 ttcagctcat gccctcaatg tttatattgt gttatctgtt gggctctggga 2050  
 catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100  
 attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150  
 caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200  
 cctagtttag aaatagggaa gotgagacat ttaagatct caagttttta 2250  
 tttactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300  
 cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350  
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 tctttttcaa gaaagagtct tttctcctt gacaaaatcc agcttttgta 2450  
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500  
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

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Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu		
35	40	45
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr		
50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu		
65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn		
80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu		
95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg		
110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp		
125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu		
140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu		
155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly		
170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser		
185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala		
200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu		
215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln		
230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys		
245	250	255
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp		
260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala		
275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys		
290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp		

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp Glu	
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly Ser	
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys Lys	
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val	Tyr Ser Gly His Gln Trp	
365	370	375
Val Asp Val His Gly Val Gln Lys Asp	Tyr Asn Val Ala Val Arg	
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His Gly	
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcggtccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaagggaggc cttcctttca gtggacccgg gtcaagaata ccac 45

<210> 300

<211> 1869

<212> DNA

<213> Homo sapiens

<400> 300

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tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150  
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cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400  
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gcacttccct atggaagtag acatattcgc cttgtcttaa aaggctcctga 800  
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 ctgtagccca aaaacaaagc cccacataaa agaggaatgc atcgtaccca 1600  
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 gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750  
 gtttaaagaa agcagtgtct cactggttgt agctttcatg gggtctgaac 1800  
 taagtgaat catctacca aagctttttg gctctcaaat taaagattga 1850  
 ttagtttcaa aaaaaaaaaa 1869

<210> 301  
 <211> 525  
 <212> PRT  
 <213> Homo sapiens

<400> 301  
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 Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu  
 20 25 30  
 Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys  
 35 40 45  
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
 50 55 60  
 Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr  
 65 70 75  
 Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala  
 80 85 90  
 Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe  
 95 100 105  
 Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser  
 110 115 120  
 Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala  
 125 130 135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe	
				425					430					435	
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val	
				440					445					450	
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp	
				455					460					465	
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro	
				470					475					480	
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro	
				485					490					495	
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln	
				500					505					510	
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser	
				515					520					525	

<210> 302  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
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 ctgggcgggg cgctgtggct ggcggcccgc cgttcgtgg ggcccagggt 150  
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 gctccaggaa gagcctagge tggatgtctt gatcaataac gcagggatct 500  
 tccagtgcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600  
 caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650  
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800  
 atcctgggtat tgtacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaaactcc 900  
 agtagaaggt gccagactt ccattttattt ggctctttca cctgaggtag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatgggt ggctgtctaa aataggaaca aggagtaaaa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatgggtg tggattgaga 1150  
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350  
 tggatgacat attaatatatt gtcagaatta agtgactcaa agtgctatcg 1400  
 agagggtttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttgggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303  
 <211> 336  
 <212> PRT  
 <213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly	1	5	10	15
Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln	20	25	30	
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr	35	40	45	
Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	50	55	60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	65	70	75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	80	85	90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly				



95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg		
110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg		
125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr		
140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His		
155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys		
170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr		
185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser		
200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile		
215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val		
230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly		
245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu		
260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr		
275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly		
290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala		
305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val		
320	325	330
Met Val Gly Leu Leu Lys		
335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100  
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250  
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300  
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
tggaaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcaggga tcttccagt cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50  
cggagcccag ccctttccta acccaacca acctagcca gtcccagccg 100  
ccagcgctg tccctgtcac ggacccagc gttaccatgc atcctgccgt 150  
cttctatcc ttaccgacc tcagatgctc cttctgctc ctggttaactt 200  
gggtttttac tctgtaca actgaaata caagtcttg tacagagaat 250  
atagatgaaa ttttaacaa tgctgatgtt gcttttagta atttttatgc 300  
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350  
ccgatgtcat taaggaaga tttccaaatg aaaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaa atgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagt accccattca agaaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650  
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataactaca aaccaccagg gcattctgct ccgatatagg 800  
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950  
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000  
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050  
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300  
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
 gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
 cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
 <211> 406  
 <212> PRT  
 <213> Homo sapiens

<400> 309  
 Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser  
 1 5 10 15  
 Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu  
 20 25 30  
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn  
 35 40 45  
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe  
 50 55 60  
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile  
 65 70 75  
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val  
 80 85 90  
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser  
 95 100 105  
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys  
 110 115 120  
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr  
 125 130 135  
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu  
 140 145 150  
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly  
 155 160 165  
 Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg  
 170 175 180  
 Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe  
 185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 48  
 <223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50  
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100  
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150  
ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
cttcctatcc ttaccgacc tcagatgctc ctttctgctc ctggtaactt 250  
gggtttttac tcctgtaaca actgaaataa cngtcttga tacnnagaat 300  
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350  
tgactgggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttccta tccttaccog acctcagatg ctcccttctg ctcttg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50  
cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100  
gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150  
taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200  
gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250  
cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300  
tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350  
catattgtca gaaggaagga tgggtgcaaat tagcttttta tcttctagca 400  
tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450  
caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500  
tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550  
tgatcagtta ctttaaaaaa tgactcctta ttttttaaata gtttccacat 600



ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700  
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 ctgttagggc tcatttttgt ttcattgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcactgtgc atgtcgatga ttatatatgg 950  
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt cttaagcata agtaaacadg atataaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaatgtgt 1150  
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200  
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaatata ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5					10					15
Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25					30
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40					45
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55					60
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70					75
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85					90
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100					105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser  
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
tgtaataccc tgaatcccct tgtactccca gactaccta tccacgcttt 100  
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150  
atatgcccct cttggcatat catatttga ggtatatgag tagaccagt 200  
atgagtggcc caggactcta tgacctaca accatcatga atgcagatat 250  
tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300  
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
tagaacaaca cacagaagaa ttggtccagt taagtgcag caaaaagcca 400  
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
gaatctgatc agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tggcgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggacccaact ggggctcccg ccgctgctgc tgctgacctat ggccttggcc 150  
ggagggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500  
 aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550  
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600  
 gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650  
 ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700  
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaaagt 750  
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
 aactcttgct ctctcggtga tggatttgc ttggatttgc tgtgcaactg 850  
 ttgctacagc tgtggagcag tatgttcct ctgagaagct gattatctat 900  
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
 ttctcttggtg gttgtagat ctaaaactga agatcatgaa gaagcagggc 1000  
 ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050  
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100  
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
 caaataaagt tactcaaact tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10				15	
Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25				30	
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40				45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55				60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70				75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85				90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100				105	

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln  
 110 115 120  
 Leu Pro Phe Ala Glu Leu Arg Gln Glu Leu Met Ser Leu Met  
 125 130 135  
 Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe  
 140 145 150  
 Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser  
 155 160 165  
 Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe  
 170 175 180  
 Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu  
 185 190 195  
 Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu  
 200 205 210  
 Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly  
 215 220 225  
 Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp  
 230 235 240  
 Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp  
 245 250 255  
 Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro  
 260 265 270  
 Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu  
 275 280 285  
 Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg  
 290 295 300  
 Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys  
 305 310 315  
 Val Asn Leu Ala His Ser Glu Ile  
 320

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50

gcacacctac cctaaggaag aggagttgta cgcattgtag agagggtgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaattcga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200  
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250  
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
tttcctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 47

<223> unknown base

<400> 332

cacactggcc ggatctttta gagtcctttg accttgacca agggctcngga 50  
aaacagcaac aagctgagct gctgtgacag aggaacaag atggcggcgc 100  
cgaagggagc ctttggtgga ggaccaact ggggctcccg ccgctgctgc 150  
tgctgaccat ggcttggcc ggagggtcgg ggaccgcttc ggctgaagca 200  
tttgactcgg tcttggtgga tacggcgtct tgccaccggg cctgtcagtt 250  
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350  
gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450  
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500  
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550  
gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

acaagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggttc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cggcccggag gtggggcgcc gctggggccg gcccgacgg gcttcactctg 100  
agggcgacag gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccgaga cagcggcaca gaggtgcttc tgccaggta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350  
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga cttttaaatc ctttggcttc tggcaagg 850  
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950  
 tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200  
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250  
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
 ttgttttaaa tgtcgtctgt ggggaaagct tcagactcag ggtttgggca 1400  
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
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 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700  
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
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Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25					30	



Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp	35	40	45
Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg	50	55	60
Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg	65	70	75
Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp	80	85	90
Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln	95	100	105
Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr	110	115	120
Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu	125	130	135
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys	140	145	150
Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe	155	160	165
Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp	170	175	180
Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp	185	190	195
Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys	200	205	210
Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln	215	220	225
Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu	230	235	240
Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His	245	250	255
Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu	260	265	270
Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln	275	280	285
Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg	290	295	300
Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu	305	310	315

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe  
 320 325 330  
 Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu  
 335 340 345  
 Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu  
 350 355 360  
 Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys  
 365 370 375  
 Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp  
 380 385 390  
 Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr  
 395 400 405  
 Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu  
 410 415 420  
 Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu  
 425 430 435  
 Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile  
 440 445 450  
 Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln  
 455 460 465  
 Asn Ile His

<210> 338  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 101, 263, 376, 397, 426  
 <223> unknown base

<400> 338  
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50  
 ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100  
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
 caagatatct ttacaagag acctggttag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtggtacca ttcttngagc gccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450  
acttcatgaa atcaagtcac ttctttgca ttttgatgag aattcatttt 500  
tttgctg 507

<210> 339  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 339  
aagctgccgg agctgcaatg 20

<210> 340  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 340  
ttgcttctta atcctgagcg c 21

<210> 341  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac tttcgactgc 20

<210> 342  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 342  
agagattcat ccaactgctcc aagtcg 26

<210> 343  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50  
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100  
ggacttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150  
cactcacctg ttcttgcccc tgggtttcct gacaggtctc tgctccccct 200  
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250  
gaatttggat acagtgtctt acaacatgtt ggggggtggac agcgatggat 300  
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350  
tttatcgctg ccctgtaggg ggggcccaca atgccccatg tgccaagggc 400  
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450  
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500  
tgagctaagg agagggtggt ggcagtgtct ctgaaggtcc ataaaagaaa 550  
aaagagaagt gtggaagg gaaaatggtct gtgtggagg gtcaaggagt 600  
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650  
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700  
gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750  
tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggatgcttc 800  
attccagcct caggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900  
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950  
gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000  
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050  
caagggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100  
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ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250  
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aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450  
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
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Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
				20					25					30
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
				35					40					45
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
				50					55					60
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
				65					70					75
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
				80					85					90
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
				95					100					105
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
				110					115					120

Phe Met Val Ser

<210> 347  
<211> 509  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22  
<223> unknown base

<400> 347  
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ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100  
ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150  
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgtcct 200  
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
tcccagggcc accagaagct gaatttgat acagtgtctt acaacatggt 300  
gggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350  
aggcgaccgg aggggggacg tttatcgctg ccctgtaggg gggggccaca 400  
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
tgggtgatgg 509

<210> 348  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 348  
agggacagag gccagaggac ttc 23

<210> 349  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 349  
caggtgcata ttcacagcag gatg 24

<210> 350  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 350  
ggaaactcccc ttctgtcactc acctgttctt gcccctgggtg ttcct 45

<210> 351  
<211> 2056  
<212> DNA  
<213> Homo sapiens

<400> 351  
aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50  
catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100  
gcttctctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
gctttatattt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250  
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
tggtttttct acgcattgat tccatgtttg ctacagatg aagtggccat 350  
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
tcttgatgtg gagccagtg atcgcgcctg gagaacagtg gtactattct 450  
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500  
ccccagcagc tgggtgctcac tcaactgaagg tcctgagtgt gatgtcactg 550  
atgacatcac ggccactgtg ccatacaacc ttctgtgtcag ggccacattg 600  
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700  
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750  
gcctactgga ggaggagcc tggtgccgag gaacatgtca aaatgggtgag 800  
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850  
actgtgtgaa ggcccagaca ttctgtgaagg ccattgggag gtacagcgcc 900  
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 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150  
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 caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250  
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 ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcattccctt 1450  
 cggctctaag ttttctcacc tgtaatgggg gaattaccta cacacctgct 1500  
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 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
 gatcaaggac tctacacact gggtggttg gagagccac tttcccagaa 1700  
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 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800  
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850  
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgtccttt tttctgttg taaagtacag 2000  
 aattcagcaa ataaaaagg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
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Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
			20						25					30



Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 35 40 45  
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
 50 55 60  
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
 65 70 75  
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
 80 85 90  
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
 95 100 105  
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
 110 115 120  
 Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser  
 125 130 135  
 Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe  
 140 145 150  
 His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe  
 155 160 165  
 Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val  
 170 175 180  
 Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met  
 185 190 195  
 Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys  
 200 205 210  
 Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu  
 215 220 225  
 Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 230 235 240  
 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp  
 245 250 255  
 Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val  
 260 265 270  
 Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
 275 280 285  
 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met  
 290 295 300  
 Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
 305 310

<210> 353  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 654, 711, 748, 827  
<223> unknown base

<400> 353  
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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200  
ccaaatgcag actttcaciaa tggttctaga agaaatctgg acaagtcttt 250  
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gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
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ggcgtgggt tgat 864

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<220>  
<223> Synthetic oligonucleotide probe

<400> 354  
aggcttcgct gcgactagac ctc 23

<210> 355  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 355  
ccaggtcggg taaggatggt tgag 24

<210> 356  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357  
<211> 1670  
<212> DNA  
<213> Homo sapiens

<400> 357  
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ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

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Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
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Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
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 65 70 75  
 Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
 80 85 90  
 Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
 95 100 105  
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 110 115 120  
 Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
 125 130 135  
 Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
 140 145 150  
 His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
 155 160 165  
 Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly  
 170 175 180  
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 185 190 195  
 Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile  
 200 205 210  
 Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu  
 215 220 225  
 Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser  
 230 235 240  
 Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile  
 245 250 255  
 Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg  
 260 265 270  
 Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser  
 275 280 285  
 Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg  
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<210> 359

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 359  
tctgctgagg tgcagctcat tcac 24

<210> 360  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 360  
gaggctctgg aagatctgag atgg 24

<210> 361  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 361  
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362  
<211> 3038  
<212> DNA  
<213> Homo sapiens

<400> 362  
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gcagctactg ctcaaaaacg ctggggcgcc caccctggca gactaacgaa 150  
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 363  
 Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu  
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 Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr  
 20 25 30



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 35 40 45  
 Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn  
 50 55 60  
 Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln  
 65 70 75  
 Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val  
 80 85 90  
 Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp  
 95 100 105  
 Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu  
 110 115 120  
 Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln  
 125 130 135  
 Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His  
 140 145 150  
 Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys  
 155 160 165  
 Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly  
 170 175 180  
 Cys Ala Ile Asn Leu Cys His Asn Met Asn Ile Trp Gly Gln Ile  
 185 190 195  
 Trp Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro Lys Gly  
 200 205 210  
 Asn Trp Trp Gly His Ala Pro Tyr Lys His Gly Arg Pro Cys Ser  
 215 220 225  
 Ala Cys Pro Pro Ser Phe Gly Gly Gly Cys Arg Glu Asn Leu Cys  
 230 235 240  
 Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr Pro Pro Arg Glu Glu Glu  
 245 250 255  
 Thr Asn Glu Ile Glu Arg Gln Gln Ser Gln Val His Asp Thr His  
 260 265 270  
 Val Arg Thr Arg Ser Asp Asp Ser Ser Arg Asn Glu Val Ile Ser  
 275 280 285  
 Ala Gln Gln Met Ser Gln Ile Val Ser Cys Glu Val Arg Leu Arg  
 290 295 300  
 Asp Gln Cys Lys Gly Thr Thr Cys Asn Arg Tyr Glu Cys Pro Ala  
 305 310 315

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr  
 320 325 330  
 Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile  
 335 340 345  
 Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg  
 350 355 360  
 Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile  
 365 370 375  
 Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr  
 380 385 390  
 Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro  
 395 400 405  
 Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg  
 410 415 420  
 Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr  
 425 430 435  
 Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His  
 440 445 450  
 Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro  
 455 460 465  
 Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
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 Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
 485 490 495  
 Val Phe Ala Val Val  
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<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag ccccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 368  
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369  
<211> 1685  
<212> DNA  
<213> Homo sapiens

<400> 369  
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agagaaagcc gagcagagct gggtagcgct tccgggcccgc cgctccgacg 150  
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gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250  
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actgcgagga gaagatgggt atcatcacca ccaagagcgt gtccaggtac 400  
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cagtgttgct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950  
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ataaaatata ttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370  
<211> 111  
<212> PRT

<213> Homo sapiens

<400> 370

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20 25 30

Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys  
35 40 45

Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
50 55 60

Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val  
65 70 75

Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln  
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Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys  
95 100 105

Arg Arg Val Tyr Glu Glu  
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<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

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<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200  
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<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn	35	40	45	
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala	50	55	60	
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro	65	70	75	
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val	80	85	90	
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu	95	100	105	
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val	110	115	120	
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro	125	130	135	
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr	140	145	150	



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Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu	
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Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser	
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Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu	
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				290					295					300	
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Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Lys	Glu	Asn	Pro	Glu	
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Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	
455		460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	
470		475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	
485		490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	
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Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	
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Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	
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Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	
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Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	
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His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	
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Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	
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Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	
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Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	
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Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn	
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Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650		655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665		670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680		685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695		700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710		715	720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys  
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp  
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg  
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr  
770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe  
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<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 377

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<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 2461

<212> DNA

<213> Homo sapiens

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Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro		50	55	60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met		65	70	75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp		80	85	90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe		95	100	105
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Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr		125	130	135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys		140	145	150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu		155	160	165
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Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met		215	220	225
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Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys		260	265	270
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu		275	280	285
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro		290	295	300
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe		305	310	315

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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 45

<212> DNA

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<211> 3150

<212> DNA

<213> Homo sapiens

<400> 384

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tttcttccaa taaaactaat tatggctcat tcccttgac aagctgtaga 2850  
actggattca tttttaaac attttcatca gtttcaaatg gtaaattctg 2900  
attgattttt aaatgcgttt ttggaagaac tttgctatta ggtagtttac 2950  
agatctttat aagggtgttt atatattaga agcaattata attacatctg 3000  
tgatttctga actaatggtg ctaattcaga gaaatggaaa gtgaaagtga 3050

gattctctgt tgtcatcggc attccaactt tttctctttg tttttgtcca 3100

gtgtttgcatt tgaatatgtc tgttttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala	
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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile	
				20					25					30	
Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys	
				35					40					45	
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro	
				50					55					60	
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu	
				65					70					75	
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser	
				80					85					90	
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val	
				95					100					105	
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala	
				110					115					120	
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His	
				125					130					135	
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser	
				140					145					150	
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu	
				155					160					165	
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu	
				170					175					180	
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp	
				185					190					195	
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr	
				200					205					210	
Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe	
				215					220					225	
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	
				230					235					240	

Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	
				245					250					255	
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	
				260					265					270	
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	
				275					280					285	
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	
				290					295					300	
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	
				305					310					315	
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	
				320					325					330	
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	
				335					340					345	
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	
				350					355					360	
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	
				365					370					375	
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	
				380					385					390	
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	
				395					400					405	
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	
				410					415					420	
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	
				425					430					435	
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	
				440					445					450	
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	
				455					460					465	
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	
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<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386  
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<210> 387  
 <211> 25  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 387  
 ttccctatgc tctgtattgg catgg 25

<210> 388  
 <211> 50  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 388  
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<210> 389  
 <211> 3313  
 <212> DNA  
 <213> Homo sapiens

<400> 389  
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 atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150  
 gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200  
 cacgcgcctg aagcaciaag cagatagcta ggaatgaacc atccctggga 250  
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 gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350  
 aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400  
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 acttgggagg ctgagtcagg agaattgctt taacctggga ggtggaggtt 3250  
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 aaactctatc tca 3313

<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu	1	5	10	15
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Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp	560	565	570



Gly Ser Thr Gly Val Glu Leu Ala Pro	Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val	Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu	Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly	Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys	Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu	Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro	Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser	Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala	Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu	Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly	Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp	Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu	Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn	Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu	Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His	Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe	Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His	Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His	Leu Cys Leu Arg Cys Asn	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	
				860					865					870	
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu	
				875					880					885	
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp	
				890					895					900	
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro	
				905					910					915	

Ala

<210> 391  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 391  
 tccgtctctg tgaaccgccc cac 23

<210> 392  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 392  
 ctcgggcgca ttgtcgttct ggtc 24

<210> 393  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 393  
 ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394  
 <211> 999  
 <212> DNA  
 <213> Homo sapiens

<400> 394  
 cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50  
 cccagttaaa aggctccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150  
 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200  
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250  
 aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttgcgagcct 300  
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 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900  
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<210> 395  
 <211> 260  
 <212> PRT  
 <213> Homo sapiens

<400> 395  
 Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu  
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 Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu  
 20 25 30  
 Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro  
 35 40 45  
 Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly  
 50 55 60  
 Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys  
 65 70 75

Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn  
 80 85 90  
 Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro  
 95 100 105  
 His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp  
 110 115 120  
 Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys  
 125 130 135  
 Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln  
 140 145 150  
 Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu  
 155 160 165  
 Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro  
 170 175 180  
 Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly  
 185 190 195  
 Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly  
 200 205 210  
 Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile  
 215 220 225  
 Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly  
 230 235 240  
 Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile  
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 Ile Gly Ser Lys Gly  
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<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

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<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaataacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

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			20						25					30	
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
			35						40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
			50						55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
			65						70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
			80						85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
			95						100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
			110						115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
			125						130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
			140						145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
			155						160					165	
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
			170						175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
			185						190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
			200						205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
			215						220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
			230						235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
			245						250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
			260						265					270	

Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val  
 275 280 285  
 Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg  
 290 295 300  
 Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro  
 305 310 315  
 Tyr His Pro Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu  
 320 325 330  
 Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser  
 335 340 345  
 Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys  
 350 355 360  
 Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly  
 365 370 375  
 Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser  
 380 385 390  
 Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro  
 395 400 405  
 Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser  
 410 415 420  
 Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly  
 425 430 435  
 Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu  
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<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcct gcgtacctc tacc 24

<210> 402

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

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<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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<210> 405

<211> 798

<212> PRT

<213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu	1	5	10	15
Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu	20	25	30	
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe	35	40	45	
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe	50	55	60	
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His	65	70	75	
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys	80	85	90	
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu	95	100	105	
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala	110	115	120	
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu	125	130	135	
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly	140	145	150	

Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala	440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser	455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser	470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp	485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn	500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln	515	520	525
Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala	530	535	540
Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn	545	550	555
Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala	560	565	570
Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu	575	580	585
Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala	590	595	600
Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe	605	610	615
Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu	620	625	630
Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys	635	640	645
Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val	650	655	660
Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu	665	670	675
Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu	680	685	690
Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val	695	700	705
Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala	710	715	720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His  
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln  
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys  
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly  
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe  
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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cggtcgacga ccgccccgcg tcatgcggt cctcggtgg tggcaagtat 150  
tgctgtgggt gctgggactt ccggtccgcg gcgtggaggt tgcagaggaa 200  
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<211> 360  
<212> PRT  
<213> Homo sapiens

<400> 410

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Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu	
				35					40					45	
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly	
				50					55					60	
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala	
				65					70					75	
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His	
				80					85					90	
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	
				95					100					105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	
				110					115					120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	
				125					130					135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	
				140					145					150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	
				155					160					165	
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Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	
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Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys	
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Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	
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Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	
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His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	
				245					250					255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly	



260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu	
275	280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys	
290	295	300
Lys Asn Val Val	Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro	
305	310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu	
320	325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu	
335	340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu	
350	355	360

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgc cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150  
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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser

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20	25	30	
Pro Asp Phe Ser Tyr	Lys Arg Ser Asn Cys Lys Pro Ile Pro Val		
35	40	45	
Asn Leu Gln Leu Cys	His Gly Ile Glu Tyr Gln Asn Met Arg Leu		
50	55	60	
Pro Asn Leu Leu Gly	His Glu Thr Met Lys Glu Val Leu Glu Gln		
65	70	75	
Ala Gly Ala Trp Ile	Pro Leu Val Met Lys Gln Cys His Pro Asp		
80	85	90	
Thr Lys Lys Phe Leu	Cys Ser Leu Phe Ala Pro Val Cys Leu Asp		
95	100	105	
Asp Leu Asp Glu Thr	Ile Gln Pro Cys His Ser Leu Cys Val Gln		
110	115	120	
Val Lys Asp Arg Cys	Ala Pro Val Met Ser Ala Phe Gly Phe Pro		
125	130	135	
Trp Pro Asp Met Leu	Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp		
140	145	150	
Leu Cys Ile Pro Leu	Ala Ser Ser Asp His Leu Leu Pro Ala Thr		
155	160	165	
Glu Glu Ala Pro Lys	Val Cys Glu Ala Cys Lys Asn Lys Asn Asp		
170	175	180	
Asp Asp Asn Asp Ile	Met Glu Thr Leu Cys Lys Asn Asp Phe Ala		
185	190	195	
Leu Lys Ile Lys Val	Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr		
200	205	210	
Lys Ile Ile Leu Glu	Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn		
215	220	225	
Gly Val Ser Glu Arg	Asp Leu Lys Lys Ser Val Leu Trp Leu Lys		
230	235	240	
Asp Ser Leu Gln Cys	Thr Cys Glu Glu Met Asn Asp Ile Asn Ala		
245	250	255	
Pro Tyr Leu Val Met	Gly Gln Lys Gln Gly Gly Glu Leu Val Ile		
260	265	270	
Thr Ser Val Lys Arg	Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg		
275	280	285	
Ile Ser Arg Ser Ile	Arg Lys Leu Gln Cys		

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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 417  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 417  
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<210> 418  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 418  
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<210> 419  
 <211> 1830  
 <212> DNA  
 <213> Homo sapiens

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 cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150  
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 ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350  
 tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

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gggagcgaat tacaagcgc cacctgaaa 1830

<210> 420  
<211> 560  
<212> PRT  
<213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg	
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Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp	
				20					25					30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	
				35					40					45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	
				50					55					60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	
				65					70					75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	
				80					85					90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	
				95					100					105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	
				110					115					120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	
				125					130					135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	
				140					145					150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	
				155					160					165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	
				170					175					180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met	
				185					190					195	
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	
				200					205					210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	
				215					220					225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	
				230					235					240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	
				245					250					255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu Leu
260	265	270
Glu Gln Ile Leu Cys	Ala Ser Gly His	Ser Ser Gly Phe Ser Gly
275	280	285
Leu Cys Gly Ala Leu	Phe Ile Thr Phe	Gly Ile Leu Gly Ala Leu
290	295	300
Ala Leu Gly Pro Tyr	Val Asp Arg Thr	Lys His Phe Thr Glu Ala
305	310	315
Thr Lys Ile Gly Leu	Cys Leu Phe Ser	Leu Ala Cys Val Pro Phe
320	325	330
Ala Leu Val Ser Gln	Leu Gln Gly Gln	Thr Leu Ala Leu Ala Ala
335	340	345
Thr Cys Ser Leu Leu	Gly Leu Phe Gly	Phe Ser Val Gly Pro Val
350	355	360
Ala Met Glu Leu Ala	Val Glu Cys Ser	Phe Pro Val Gly Glu Gly
365	370	375
Ala Ala Thr Gly Met	Ile Phe Val Leu	Gly Gln Ala Glu Gly Ile
380	385	390
Leu Ile Met Leu Ala	Met Thr Ala Leu	Thr Val Arg Arg Ser Glu
395	400	405
Pro Ser Leu Ser Thr	Cys Gln Gln Gly	Glu Asp Pro Leu Asp Trp
410	415	420
Thr Val Ser Leu Leu	Leu Met Ala Gly	Leu Cys Thr Phe Phe Ser
425	430	435
Cys Ile Leu Ala Val	Phe Phe His Thr	Pro Tyr Arg Arg Leu Gln
440	445	450
Ala Glu Ser Gly Glu	Pro Pro Ser Thr	Arg Asn Ala Val Gly Gly
455	460	465
Ala Asp Ser Gly Pro	Gly Val Asp Arg	Gly Gly Ala Gly Arg Ala
470	475	480
Gly Val Leu Gly Pro	Ser Thr Ala Thr	Pro Glu Cys Thr Ala Arg
485	490	495
Gly Ala Ser Leu Glu	Asp Pro Arg Gly	Pro Gly Ser Pro His Pro
500	505	510
Ala Cys His Arg Ala	Thr Pro Arg Ala	Gln Gly Pro Ala Ala Thr
515	520	525
Asp Ala Pro Ser Arg	Pro Gly Arg Leu	Ala Gly Arg Val Gln Ala
530	535	540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
545 550 555

Pro Trp Val Ile Thr  
560

<210> 421  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 421  
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<210> 422  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 422  
cggttcaata aacctggacg cttgg 25

<210> 423  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 423  
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<210> 424  
<211> 4313  
<212> DNA  
<213> Homo sapiens

<400> 424  
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tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150  
tggccttgcc ttggggtoct gcttgtttca taatcatcta actatgggac 200  
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 aaaaaaaaaa aaa 4313

<210> 425  
 <211> 1184  
 <212> PRT  
 <213> Homo sapiens

<400> 425  
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Thr Val Lys Tyr	Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu	Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala	Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val	Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg	Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp	Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln	Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu	Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile	Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu	His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe	170	175	180
Ala Leu Asp Val	Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val	Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg	Pro Leu Asp Tyr	Glu Lys Asn
305		310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly	Pro Asn
320		325	330
Pro Ile Pro Ala	His Cys Lys Val	Leu Ile Lys Val	Leu Asp Val
335		340	345
Asn Asp Asn Ile	Pro Ser Ile His	Val Thr Trp Ala	Ser Gln Pro
350		355	360
Ser Leu Val Ser	Glu Ala Leu Pro	Lys Asp Ser Phe	Ile Ala Leu
365		370	375
Val Met Ala Asp	Asp Leu Asp Ser	Gly His Asn Gly	Leu Val His
380		385	390
Cys Trp Leu Ser	Gln Glu Leu Gly	His Phe Arg Leu	Lys Arg Thr
395		400	405
Asn Gly Asn Thr	Tyr Met Leu Leu	Thr Asn Ala Thr	Leu Asp Arg
410		415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu	Thr Leu Leu Ala	Gln Asp Gln
425		430	435
Gly Leu Gln Pro	Leu Ser Ala Lys	Lys Gln Leu Ser	Ile Gln Ile
440		445	450
Ser Asp Ile Asn	Asp Asn Ala Pro	Val Phe Glu Lys	Ser Arg Tyr
455		460	465
Glu Val Ser Thr	Arg Glu Asn Asn	Leu Pro Ser Leu	His Leu Ile
470		475	480
Thr Ile Lys Ala	His Asp Ala Asp	Leu Gly Ile Asn	Gly Lys Val
485		490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro	Val Ala His Leu	Val Ala Ile
500		505	510
Asp Ser Asn Thr	Gly Glu Val Thr	Ala Gln Arg Ser	Leu Asn Tyr
515		520	525
Glu Glu Met Ala	Gly Phe Glu Phe	Gln Val Ile Ala	Glu Asp Ser
530		535	540
Gly Gln Pro Met	Leu Ala Ser Ser	Val Ser Val Trp	Val Ser Leu
545		550	555
Leu Asp Ala Asn	Asp Asn Ala Pro	Glu Val Val Gln	Pro Val Leu
560		565	570
Ser Asp Gly Lys	Ala Ser Leu Ser	Val Leu Val Asn	Ala Ser Thr
575		580	585

Gly His Leu Leu Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro	590	595	600
Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro		605	610	615
Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala		620	625	630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His		635	640	645
Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val		650	655	660
Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile		665	670	675
Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu		680	685	690
Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser		695	700	705
Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile		710	715	720
Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu		725	730	735
Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr		740	745	750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg		755	760	765
Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val		770	775	780
Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His		785	790	795
Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro		800	805	810
Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr		815	820	825
Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu		830	835	840
Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln		845	850	855
Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro		860	865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser  
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 Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro  
 890 895 900  
 Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His  
 905 910 915  
 Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln  
 920 925 930  
 Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu  
 935 940 945  
 Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln  
 950 955 960  
 Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln  
 965 970 975  
 Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly  
 980 985 990  
 Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg  
 995 1000 1005  
 Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp  
 1010 1015 1020  
 Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu  
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 Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu  
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 Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu  
 1055 1060 1065  
 Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala  
 1070 1075 1080  
 Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala  
 1085 1090 1095  
 Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val  
 1100 1105 1110  
 Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser  
 1115 1120 1125  
 Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser  
 1130 1135 1140  
 Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala  
 1145 1150 1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr  
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu  
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

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<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

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<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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tgagtttctt catcgactcc agcatcatga ttacctcca gatactattt 200  
tttggatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250  
gatacgtcag tatgttgtac aggtgatctt ctccgtgacg tttgcatttt 300



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<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe	20	25	30	
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser	35	40	45	
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe	50	55	60	
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp	65	70	75	
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val	80	85	90	
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu	95	100	105	
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe	110	115	120	
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	125	130	135	
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	140	145	150	
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	155	160	165	
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	170	175	180	
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln				

185	190	195
Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala 200	205	210
Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser 215	220	225
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly 230	235	240
Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu 245	250	255
Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala 260	265	270
Thr Lys Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr 275	280	285
Phe Asn Phe Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys 290	295	300
Ile Phe Met Ala Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys 305	310	315
Thr Asp Pro Val Thr Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu 320	325	330
Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe 335	340	345
Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu 350	355	360
Ile Thr Leu Thr Lys Phe Phe Tyr Ala Ile Ser Ser Ser Lys Ser 365	370	375
Ser Asn Val Ile Val Leu Leu Leu Ala Gln Ile Met Gly Met Tyr 380	385	390
Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser Met Pro Leu Glu 395	400	405
Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu Gln Phe Asn 410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu 425	430	435
Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu 440	445	450
Lys Gln Met Ala Pro 455		

<210> 431

<211> 407  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 81, 113, 157, 224, 297  
<223> unknown base

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tggcttttct tcnegccaa tgtttaaaga ctatgagata cgtcagtatg 150  
ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200  
gagctcatca tctttgaaat cttnggagta ttgaatagca gctcccgta 250  
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tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350  
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400  
ttccag 407

<210> 432  
<211> 457  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434  
<223> unknown base

<400> 432  
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catttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250  
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tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400  
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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttgttta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgtttaaa gactatgaga tacgtcagta tggtgtacag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

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 a 3951

<210> 437  
 <211> 1141  
 <212> PRT  
 <213> Homo sapiens

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 Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu  
 35 40 45  
 Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg  
 50 55 60  
 Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro  
 65 70 75  
 Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly  
 80 85 90  
 Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg  
 95 100 105



Val Asp Ile Asp Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu Gly Val Ser Val Arg	Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala	380	385	390

Val Leu Gly Asp Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val  
 395 400 405  
 Gly Ala Pro Phe Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly  
 410 415 420  
 Ser Ser Leu Gly Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly  
 425 430 435  
 Glu Ala Val Gly Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser  
 440 445 450  
 Leu Asp Met Asp Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser  
 455 460 465  
 Leu Ala Asp Thr Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His  
 470 475 480  
 Val Ser His Glu Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu  
 485 490 495  
 Gln Pro Asn Cys Ala Gly Gly His Ser Val Cys Val Asp Leu Arg  
 500 505 510  
 Val Cys Phe Ser Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr  
 515 520 525  
 Val Ala Leu Asp Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu  
 530 535 540  
 Arg Gly Gln Val Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu  
 545 550 555  
 Glu Pro Lys His Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln  
 560 565 570  
 His Asp Arg Val Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn  
 575 580 585  
 Val Lys Asp Lys Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser  
 590 595 600  
 Leu Gln Thr Pro Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu  
 605 610 615  
 Pro Pro Val Ala Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln  
 620 625 630  
 Arg Ala Glu Ile His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys  
 635 640 645  
 Ile Cys Gln Ser Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr  
 650 655 660  
 Arg Val Ser Asp Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp  
 665 670 675

Gly Thr Thr Ala Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly	680	685	690
Leu Glu Leu Met Val Thr Asn Leu Pro Ser Asp Pro Ala Gln Pro		695	700	705
Gln Ala Asp Gly Asp Asp Ala His Glu Ala Gln Leu Leu Val Met		710	715	720
Leu Pro Asp Ser Leu His Tyr Ser Gly Val Arg Ala Leu Asp Pro		725	730	735
Ala Glu Lys Pro Leu Cys Leu Ser Asn Glu Asn Ala Ser His Val		740	745	750
Glu Cys Glu Leu Gly Asn Pro Met Lys Arg Gly Ala Gln Val Thr		755	760	765
Phe Tyr Leu Ile Leu Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr		770	775	780
Glu Leu Glu Val Glu Leu Leu Leu Ala Thr Ile Ser Glu Gln Glu		785	790	795
Leu His Pro Val Ser Ala Arg Ala Arg Val Phe Ile Glu Leu Pro		800	805	810
Leu Ser Ile Ala Gly Met Ala Ile Pro Gln Gln Leu Phe Phe Ser		815	820	825
Gly Val Val Arg Gly Glu Arg Ala Met Gln Ser Glu Arg Asp Val		830	835	840
Gly Ser Lys Val Lys Tyr Glu Val Thr Val Ser Asn Gln Gly Gln		845	850	855
Ser Leu Arg Thr Leu Gly Ser Ala Phe Leu Asn Ile Met Trp Pro		860	865	870
His Glu Ile Ala Asn Gly Lys Trp Leu Leu Tyr Pro Met Gln Val		875	880	885
Glu Leu Glu Gly Gly Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser		890	895	900
Pro Arg Pro Asn Ile Leu His Leu Asp Val Asp Ser Arg Asp Arg		905	910	915
Arg Arg Arg Glu Leu Glu Pro Pro Glu Gln Gln Glu Pro Gly Glu		920	925	930
Arg Gln Glu Pro Ser Met Ser Trp Trp Pro Val Ser Ser Ala Glu		935	940	945
Lys Lys Lys Asn Ile Thr Leu Asp Cys Ala Arg Gly Thr Ala Asn		950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala  
 965 970 975  
 Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu  
 980 985 990  
 Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn  
 995 1000 1005  
 Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala  
 1010 1015 1020  
 Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val  
 1025 1030 1035  
 Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu  
 1040 1045 1050  
 Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys  
 1055 1060 1065  
 Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro  
 1070 1075 1080  
 Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe  
 1085 1090 1095  
 Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser  
 1100 1105 1110  
 Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp  
 1115 1120 1125  
 Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr  
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Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgcctct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200  
ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250  
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acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350  
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400  
tgcttaaaga tgaaatgtag tcgccataaa gtagtcattg ctcaagattc 450  
tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500  
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550  
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cccaccagta caagcagaaa tgttaagaga gcatgcagt acctggagtt 750  
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 aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050  
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 tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250  
 gaataaatgg tgttgcatag tgtgctatag attttgagat ctccggagat 1300  
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 cctattttaa attatcttct tcccaataa caaatgatt ctaaacctca 1550  
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 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850  
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900  
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 aaaaaaaaaa aaaa 1964

<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

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Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20					25					30

Gly	Arg	Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
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Phe Arg Asp Glu Val Glu Asp Asp Tyr Phe Arg Thr Trp Ser Pro 65 70 75		
Gly Lys Pro Phe Asp Gln Ala Leu Asp Pro Ala Lys Asp Pro Cys 80 85 90		
Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp 95 100 105		
Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg 110 115 120		
Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile 125 130 135		
Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val 140 145 150		
Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu 155 160 165		
Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu 170 175 180		
Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg 185 190 195		
Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala 200 205 210		
Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser 215 220 225		
Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg 230 235 240		
Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp 245 250 255		
Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln 260 265 270		
Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr 275 280 285		
Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile 290 295 300		
Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro 305 310 315		
Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val		

320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro	Leu Cys Asp Glu Asp Gly	
335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly	Ser Val Gly Gln Cys Trp	
350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val	Met Gly Ser Arg Ile Asn	
365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe	Glu Ile Ser Gly Asp Phe	
380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr	Asp Asp Glu Asp Asp Glu	
395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu	Ile Glu Asp Asp Asp Glu	
410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly	Asp Asp His Asp Val Tyr	
425	430	435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatgggc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445



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<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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cagggatggg cgacaagatc tggctgccct tccccgtgct ccttctggcc 150  
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ctgaagttgg tgattacatg ttctgctttg acaatacatt cagcaccatt 450  
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ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550  
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<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225
Lys Ser Arg Thr			

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

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<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgtcgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

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gccctgcca gtgtgtcctg gatgctgctt tctgcctca ttctcctgtg 150  
tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200  
gctgtcccaa aggtccaag gcctatggct cccctgcta tgccttgttt 250  
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cctccctggg gaggagcatt agtaacagct actatacat ctggattggg 400  
ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450  
gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500  
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ttctcccaa actgccctac ctgactacct tgtcatgac ctccttcttt 750  
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gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850  
aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT

<213> Homo sapiens

<400> 452

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu  
1 5 10 15  
Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
20 25 30  
Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
35 40 45  
Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser  
50 55 60  
Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys  
65 70 75  
Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser  
80 85 90  
Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly  
95 100 105  
Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp  
110 115 120  
Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys  
125 130 135  
Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser  
140 145 150  
Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala  
155 160 165  
Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp  
170 175

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

ccagtctgtc gccacctcac ttggtgtctg ctgtccccgc caggcaagcc 50  
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ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150  
tgcgctgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200  
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250  
ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgccccg 400  
 tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450  
 tccgactgta gagtccccgc ccacccccat ggccctatgc ggcccagccc 500  
 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaa aaaaaaaaaa 550

<210> 454  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 454  
 Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
 1 5 10 15  
 Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
 20 25 30  
 Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
 35 40 45  
 Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
 50 55 60  
 Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
 65 70 75  
 Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
 80 85 90  
 Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
 95 100 105  
 Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
 110 115 120  
 Leu Ser Leu Arg Leu  
 125

<210> 455  
 <211> 1518  
 <212> DNA  
 <213> Homo sapiens

<400> 455  
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 agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100  
 attttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150  
 gcgcagcggg agctaccggt gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250  
ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300  
accaggtc tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350  
aataagtacc agaccattga caactaccag ccgtaccctg gcgcagagga 400  
cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450  
acgcaggcgt gcaaactctgt ctgcctgca ggaagcgccg aaaacgctgc 500  
atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600  
ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650  
accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700  
ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750  
tctggtcaa gatctgtaaa cctgtcctga aagaaggta agtgtgtacc 800  
aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850  
ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900  
gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950  
aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000  
ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050  
gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100  
ttatggaact cccctgtgat tgcagtaaata tactgtattg taaattctca 1150  
gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200  
ggtgctgcac tgctatttt tctcttgtt atgtaaattt ttgtacacat 1250  
tgattgttat cttgactgac aaatattcta tattgaactg aagtaaatca 1300  
tttcagctta tagttcttaa aagcataacc ctttacccta ttaattcta 1350  
gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400  
atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450  
ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500  
catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266



<212> PRT

<213> Homo sapiens

<400> 456

Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala  
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Met Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser  
20 25 30  
Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
35 40 45  
Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
50 55 60  
Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
65 70 75  
Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu  
80 85 90  
Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp  
95 100 105  
Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg  
110 115 120  
Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn  
125 130 135  
Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile  
140 145 150  
Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu  
155 160 165  
Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His  
170 175 180  
Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys  
185 190 195  
Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys  
200 205 210  
Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg  
215 220 225  
Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly  
230 235 240  
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser  
245 250 255  
Asn Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265

<210> 457  
<211> 638  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,  
509, 556  
<223> unknown base

<400> 457  
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catttttttt tctttctcct tcnggagtcc ttntgagang atggtttttg 150  
gcgcagcggg agctaaccgc gttttttgtn gcgatggtag cggcggtttt 200  
cggcggccac cttntgctgg gagtgagcgc caccttgaat cggttttcaa 250  
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accaggnnt tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350  
aataagtacc agaccattga caattaccag ccgtaccgt gcgcagagga 400  
cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450  
angcgggcgt gcaaatntgt ntngcctgca ggaagcgccg aaaacgctgc 500  
atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600  
ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458  
<211> 4040  
<212> DNA  
<213> Homo sapiens

<400> 458  
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ttctctcctg cacgcggtgc ttgggctcgg ccaggcgggg tccgccgcca 150  
gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200  
gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250  
ttcacagatt aatatTTTT gggacagatt tgtgatgctt gattcaccct 300

tgaagtaatg tagacagaag ttctcaaatt tgcattattac atcaactgga 350  
accagcagtg aatcttaatg ttactttaaa tcagaacttg cataagaaag 400  
agaatgggag tctgggttaaa taaagatgac tatatcagag acttgaaaag 450  
gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500  
atcaggattt ttacagttta cttggagtgt ccaaaactgc aagcagtaga 550  
gaaataagac aagctttcaa gaaattggca ttgaagttac atcctgataa 600  
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catatgaagt actcaaagat gaagatctac ggaaaaagta tgacaaatat 700  
ggagaaaagg gacttgagga taatcaaggt ggccagtatg aaagctggaa 750  
ctattatcgt tatgattttg gtatttatga tgatgacct gaaatcataa 800  
cattggaaag aagagaattt gatgctgctg ttaattctgg agaactgtgg 850  
tttgtaaatt ttactcccc aggctgttca cactgccatg atttagctcc 900  
cacatggaga gactttgcta aagaagtgga tgggttactt cgaattggag 950  
ctgttaactg tggatgatgat agaatgcttt gccgaatgaa aggagtcaac 1000  
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ttagaagtac agtgacagaa ctttggacag gaaattttgt caactccata 1150  
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caaatgatcc tgagctgaaa aaactaaaaa ctctacttaa aaatgatcat 1450  
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tctgtatgtt tttcagccgt ctctagcagt atttaaagga caaggaacca 1550  
aagaatatga aattcatcat ggaaagaaga ttctatatga tatacttgcc 1600  
tttgccaaag aaagtgtgaa ttctcatgtt accacgcttg gacctcaaaa 1650  
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ggtgtccacc atgtcgagct ttactaccag agttacgaag agcatcaa 1750

cttctttatg gtcagcttaa gtttgggtaca ctagattgta cagttcatga 1800  
gggactctgt aacatgtata acattcaggc ttatccaaca acagtgggtat 1850  
tcaaccagtc caacattcat gagtatgaag gacatcactc tgctgaacaa 1900  
atcttggagt tcatagagga tcttatgaat ccttcagtgg tctcccttac 1950  
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cttggttagg atgattaaag gaaaagtga agctggaaaa gtagactgtc 2450  
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gataaatacc agagatgcaa aagcaatcgc tgccttaata agtgaaaaat 2600  
tggaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650  
tgttgaagat gaagaaaaag tttaaaagaa attctgacag atgacatcag 2700  
aagacaccta tttagaatgt tacatttatg atgggaatga atgaacatta 2750  
tcttagactt gcagttgtac tgccagaatt atctacagca ctggtgtaaa 2800  
agaaggggtct gcaaactttt tctgtaaagg gccggtttat aaatatttta 2850  
gactttgcag gctataatat atggttcaca catgagaaca agaataagat 2900  
catcatgtat tctttgttat ttgcttttaa caacctttaa aaaatattaa 2950  
aacgattctt agctcagagc catacaaaag taggctggat tcagtccatg 3000  
gaccatagat tgctgtcccc ctgcacggac ttataatgtt tcaggtggct 3050  
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 aaggttgaaa aaatgctttt aatttttcac agccgagaaa cagtgcagca 3350  
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 tagagttcta tattttaaag atatatgtgt tcatgtattt tctgaaattg 3550  
 ctttcataga aattttccca ctgatagttg atttttgagg catctaatat 3600  
 ttacatatatt gccttctgaa ctttggtttg acctgtatcc tttatttaca 3650  
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 aatgatactg tagttattcc agttactagt ttactgtcag agggctgcct 3800  
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 attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaaa 4040

<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys
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Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
			20						25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu  
 80 85 90  
 Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu  
 95 100 105  
 Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr  
 110 115 120  
 Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu  
 125 130 135  
 Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe  
 140 145 150  
 Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala  
 155 160 165  
 Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg  
 170 175 180  
 Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met  
 185 190 195  
 Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly  
 200 205 210  
 Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu  
 215 220 225  
 Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu  
 230 235 240  
 Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala  
 245 250 255  
 Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys  
 260 265 270  
 Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu  
 275 280 285  
 Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn  
 290 295 300  
 Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg  
 305 310 315  
 Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn  
 320 325 330  
 Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu  
 335 340 345  
 Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala  
 350 355 360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala  
 365 370 375  
 Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly  
 380 385 390  
 Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val  
 395 400 405  
 Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn  
 410 415 420  
 Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro  
 425 430 435  
 Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu  
 440 445 450  
 Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His  
 455 460 465  
 Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr  
 470 475 480  
 Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His  
 485 490 495  
 Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro  
 500 505 510  
 Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr  
 515 520 525  
 Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro  
 530 535 540  
 Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met  
 545 550 555  
 Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys  
 560 565 570  
 Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr  
 575 580 585  
 Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln  
 590 595 600  
 Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg  
 605 610 615  
 Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr  
 620 625 630  
 Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp  
 635 640 645

Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe  
 650 655 660  
 Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val  
 665 670 675  
 Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln  
 680 685 690  
 Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr  
 695 700 705  
 Glu Arg Ala Lys Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg  
 710 715 720  
 Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr  
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 Leu Arg Asn Gln Gly Lys Arg Asn Lys Asp Glu Leu  
 740 745

<210> 460  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 461  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 461  
 gatcagccag ccaataccag cagc 24

<210> 462  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 462  
 gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463  
 <211> 1818  
 <212> DNA



<213> Homo sapiens

<400> 463

agacagtacc tcctccctag gactacacaa ggactgaacc agaaggaaga 50  
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caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcctc 150  
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200  
catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat 250  
attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300  
agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc 350  
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400  
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgac 450  
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500  
ctaggacatt tttagatcac aaaagcactt cttccatcga tgatggagag 550  
aatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600  
ttccttacct catcccatat tgttccagca aatttgccgc tgttggtttt 650  
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700  
aacctcatgt ctctgcccag tttttgtgaa tactgggttc accaaaaatc 750  
caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800  
ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgt 850  
tatcaatatc tttctgagac tacagaagtt tcttcctgaa cgcgcctcag 900  
cgattttaaa tcgtatgcag aatattcaat ttgaagcagt ggttgccac 950  
aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000  
ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050  
tttttcagtc ctgataatat taaaaacatt ggtttggcac tagcagcagt 1100  
caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatttac 1150  
gtagtttttc ataggtctgt ttttccttcc atgcctctta aaaacttctg 1200  
tgcttacata aacatactta aaagggttttc tttaagatat tttatttttc 1250  
catttaaagg tggacaaaag ctacctccct aaaagtaaat acaaagagaa 1300  
cttatttaca caggggaaggt ttaagactgt tcaagtagca ttccaatctg 1350

tagccatgcc acagaatatc aacaagaaca cagaatgagt gcacagctaa 1400  
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450  
 attcagcatt tgaagattt ccctagcctc ttcctttttc attagcccaa 1500  
 aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550  
 aactctgaag tccacaaaaa gtggaccctc tatatttcct ccctttttat 1600  
 agtcttataa gatacattat gaaagggtgac cgactctatt ttaaatctca 1650  
 gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700  
 ttcatatatc cttgggtccca gagatgttta gacaatttta ggctcaaaaa 1750  
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800  
 atggacccaa gagaagaa 1818

<210> 464  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
 Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile  
 1 5 10 15  
 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg  
 20 25 30  
 Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly  
 35 40 45  
 His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln  
 50 55 60  
 Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu  
 65 70 75  
 Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr  
 80 85 90  
 Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn  
 95 100 105  
 Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn  
 110 115 120  
 Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu  
 125 130 135  
 Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp  
 140 145 150  
 Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly



aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600  
cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650  
gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700  
cgcggtgcgc cctaccgga cccgctgcgc atcccgcgcg agcacgtgca 750  
caacgccagc gcgcacctga ccttcaacaa gttctggcgc cgctacggga 800  
agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850  
ctcttcgtgc gcgaccctt cgtgcgcctg atctccgct tccgcagcaa 900  
gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccattg 950  
tgcggtgta cgccaaccac accagcctgc ccgctcggc gcgcgaggcc 1000  
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tgtaccgct ctgccaccg tgccagatcg actacgactt cgtggggaag 1150  
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gctgggagga ggactggttc gccaagatcc cctgggcctg gaggcagcag 1300  
ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350  
cgaaaacctc ctccgagact gaaagcttcc gcgttgcttt ttctcgcgtg 1400  
cctggaacct gacgcacgcg cactccagtt tttttatgac ctacgatttt 1450  
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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
			20						25				30	

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
			35						40				45	

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
			50						55				60	

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser  
 65 70 75  
 Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln  
 80 85 90  
 Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp  
 95 100 105  
 Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln  
 110 115 120  
 Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser  
 125 130 135  
 Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro  
 140 145 150  
 Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala  
 155 160 165  
 Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg  
 170 175 180  
 Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro  
 185 190 195  
 Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala  
 200 205 210  
 Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys  
 215 220 225  
 Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys  
 230 235 240  
 Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe  
 245 250 255  
 Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe  
 260 265 270  
 Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro  
 275 280 285  
 Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe  
 290 295 300  
 Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu  
 305 310 315  
 Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His  
 320 325 330  
 Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu  
 335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
 350 355 360  
 Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
 365 370 375  
 Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
 380 385 390  
 Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
 395 400 405  
 Pro Lys Pro Glu Asn Leu Leu Arg Asp  
 410

<210> 467  
 <211> 1071  
 <212> DNA  
 <213> Homo sapiens

<400> 467  
 tcgggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50  
 ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100  
 acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150  
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200  
 cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250  
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300  
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350  
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400  
 ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450  
 ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500  
 tcaaggaat gtcataca tctccagcct ggtgggggca atcggccagg 550  
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
 aaagcttttg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650  
 ctccccagga aacatctgga ccccgtgtg ggaggagctg gcagccttaa 700  
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
 ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttcctggc 800  
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850  
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900

cccgatatcc cttcctgatt tctctcattt ctacttgggg ccccttcct 950  
 aggactctcc caccctaaac tccaacctgt atcagatgca gcccccaagc 1000  
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcagggttc 1050  
 ccataaaaac gatttgcagc c 1071

<210> 468  
 <211> 270  
 <212> PRT  
 <213> Homo sapiens

<400> 468

Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr  
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 Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val  
 20 25 30  
 Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly  
 35 40 45  
 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu  
 50 55 60  
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu  
 65 70 75  
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala  
 80 85 90  
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln  
 95 100 105  
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr  
 110 115 120  
 Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn  
 125 130 135  
 Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln  
 140 145 150  
 Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr  
 155 160 165  
 Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn  
 170 175 180  
 Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu  
 185 190 195  
 Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met  
 200 205 210

Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly  
 215 220 225  
 Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly  
 230 235 240  
 Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys  
 245 250 255  
 Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser  
 260 265 270

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
 aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50  
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100  
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgagggtca 300  
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350  
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
 gcatggtgag cgtgccggtg ttcagccagg ttctgtgcg ccgccgcctc 500  
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550  
 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
 gccaggccag cagcccagaa ccattcctct tgcacctttg tgccaagaaa 650  
 ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 470  
 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile  
 1 5 10 15  
 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
 20 25 30



Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val	
				35					40					45	
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu	
				50					55					60	
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn	
				65					70					75	
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu	
				80					85					90	
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile	
				95					100					105	
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg	
				110					115					120	
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp	
				125					130					135	
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg	
				140					145					150	
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln	
				155					160					165	
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe	
				170					175					180	

<210> 471  
 <211> 2368  
 <212> DNA  
 <213> Homo sapiens

<400> 471  
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 aaaccgggag ggcgagcgag gctgcggggc ggccgctgcc cttccccaca 100  
 ctccccgccg agaagcctcg ctgcggcccc aacatggcgg gtgggcgctg 150  
 cggcccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200  
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250  
 cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300  
 gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350  
 aatgggaggg ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400  
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450  
 cactctccca gcattttttc atgcaaagga tgggatattc cgccgttata 500

gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550  
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600  
gatgtctgga atggctggtc ttttagcat ctctggcaag atatggcatc 650  
ttcacaacta tttcacagtg actcttggaa ttcctgcttg gtgttcttat 700  
gtgtttttcg tcatagccac cttgggtttt ggccttttta tgggtctggt 750  
cttggtggtta atatcagaat gtttctatgt gccacttcca aggcatttat 800  
ctgagcgttc tgagcagaat cggagatcag aggaggctca tagagctgaa 850  
cagttgcagg atgcggagga ggaaaaagat gattcaaatg aagaagaaaa 900  
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950  
aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctggtgtg 1000  
gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050  
tgtgaccogg gaggaagtag agcctgagga ggctgaagaa ggcatctctg 1100  
agcaaccctg cccagctgac acagagggtg tggaagactc cttgaggcag 1150  
cgtaaaagtc agcatgctga caagggactg tagatttaat gatgcgtttt 1200  
caagaatata caccaaaaca atatgtcagc ttccctttgg cctgcagttt 1250  
gtaccaaate ctttaattttt cctgaatgag caagcttctc ttaaaagatg 1300  
ctctctagtc atttgggtctc atggcagtaa gcctcatgta tactaaggag 1350  
agtcttccag gtgtgacaat caggatatag aaaaacaaac gtagtgtttg 1400  
gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450  
agagtctoga ccagaggagg ccattcccag tcctaatacag caccttccag 1500  
agacaaggct gcaggccctg tgaaatgaaa gccaagcagg agccttggt 1550  
cctgagcatc ccaaagtgt aacgtagaag ccttgcattc ttttcttggt 1600  
taaagtattt atttttgtca aattgcagga aacatcaggc accacagtgc 1650  
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cagctcagaa gtcattcccag ccctctgaat ctctgtgct atgttttatt 1750  
tcttaccttt aatttttcca gcatttccac catgggcatt caggctctcc 1800  
acactcttca ctattatctc ttggtcagag gactccaata acagccagg 1850  
ttacatgaac tgtgtttgtt cattctgacc taaggggttt agataatcag 1900  
taaccataac ccctgaagct gtgactgcca aacatctcaa atgaaatgtt 1950

gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000  
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050  
 tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100  
 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcattctcaag 2150  
 gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200  
 gattttcctt cagtgatgtg cttttgtga aagaattaat gaactccagt 2250  
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300  
 agaattatat ctttgtaaatt ctctcaatac tcaatctact gtaagtaccc 2350  
 agggaggcta atttcttt 2368

<210> 472  
 <211> 349  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
 Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala  
 1 5 10 15  
 Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala  
 20 25 30  
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
 35 40 45  
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
 50 55 60  
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
 65 70 75  
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
 80 85 90  
 Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val  
 95 100 105  
 Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg  
 110 115 120  
 Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile  
 125 130 135  
 Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys  
 140 145 150  
 Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser  
 155 160 165

Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr  
 170 175 180  
 Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala  
 185 190 195  
 Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile  
 200 205 210  
 Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg  
 215 220 225  
 Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln  
 230 235 240  
 Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu  
 245 250 255  
 Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu  
 260 265 270  
 Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu  
 275 280 285  
 Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly  
 290 295 300  
 Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu  
 305 310 315  
 Glu Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr  
 320 325 330  
 Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala  
 335 340 345  
 Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

gtccagccca tgaccgcctc caac 24

<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctcctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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gccacatga ttgactcag agattctctt ttgtccacag acagtcatct 100  
caggggcaga aagaaaagag ctcccaaag ctatatctat tcaggggctc 150  
tcaagaacaa tggaatatca tcttgattta gaaaatttgg atgaagatgg 200  
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250  
tttcagagaa aggatcgtgt gctgcatctc ctcttggcg cctcattgct 300  
gtaattttgg gaatcctatg cttggtaata ctgggtgatag ctgtggctct 350  
gggtaccatg ggggttcttt ccagcccttg tctctctaatt tggattatat 400  
atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450  
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ctcaaatgaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550  
attcattttg gataggcctt tctcggtccc agactgaggt accatggctc 600  
tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650  
agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700  
tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750  
aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800  
gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgaggtca 850  
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cagccaagct tgagttttta ttttttattt atttattttt ttgagatagg 1050  
gtctcacttt gttaccagg ctggagtgc gtggcacaat ctgactcac 1100  
tgcagctatc tctcgctca gcccctcaag tagctgggac tacaggtgca 1150  
tgccaccatg ccaggctaata ttttggtgtt tttttagag actgggtttt 1200  
gcatgttga ccaagctggt ctctaactcc tgggcttaag tgatctgccc 1250  
gccttggcct cccaaagtgc tgggattaca gatgtgagcc accacacctg 1300  
gccccaaagct tgaattttca ttctgccatt gacttggcat ttaccttggg 1350  
taagccataa gcgaatctta atttctggct ctatcagagt tgtttcatgc 1400  
tcaacaatgc cattgaagtgc cagggtgtgt tgccacgatt tgacctcaa 1450  
cttctagcag tatatcagtt atgaactgag ggtgaaatat atttctgaat 1500  
agctaaatga agaaatggga aaaaatcttc accacagtca gagcaatttt 1550  
attattttca tcagtatgat cataattatg attatcatct tagtaaaaag 1600  
caggaactcc tactttttct ttatcaatta aatagctcag agagtacatc 1650  
tgccatatct ctaatagaat cttttttttt tttttttttt tttgagacag 1700  
agtttcgctc ttgttgccca ggctggagtgc caacggcacg atctcggtc 1750  
accgcaacct ccgccccctg ggtcaagca attctctgc ctgacctcc 1800  
caagtagctg ggattacagt caggcaccac cacaccggc taattttgta 1850  
tttttttagt agagacaggg tttctccatg tcggtcaggg tagtcccgaa 1900  
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acaggcgtga gccactgcac ccagcctaga atcttgtata atatgtaatt 2000  
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<212> PRT

<213> Homo sapiens

<400> 477

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Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile  
50 55 60

Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro  
65 70 75

Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met  
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Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu  
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Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe  
110 115 120

Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile  
125 130 135

Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp  
140 145 150

Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala  
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Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser  
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<210> 483  
 <211> 693  
 <212> PRT  
 <213> Homo sapiens

<400> 483

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				20					25					30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
				35					40					45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
				50					55					60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
				65					70					75
Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe
				80					85					90

Cys Leu Tyr Trp Asn Arg His Ala Gly Arg Leu His Leu Leu Tyr	95	100	105
Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala Ser Ser Leu Leu	110	115	120
Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly Pro Pro Leu	125	130	135
Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn Ile Ser	140	145	150
Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro Pro	155	160	165
His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys	170	175	180
Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys	185	190	195
Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln	200	205	210
Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met	215	220	225
Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu	230	235	240
Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln	245	250	255
Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro	260	265	270
Arg Thr Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu	275	280	285
Lys Arg Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln	290	295	300
Asp Lys Asn Ser Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile	305	310	315
Val Val Gln Asn Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val	320	325	330
Leu Thr Phe Gln His Gln Leu Gln Pro Lys Asn Val Thr Leu Gln	335	340	345
Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser Ser Pro Gly His	350	355	360
Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu Thr Gln Thr	365	370	375

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 Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu  
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 Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly  
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 Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe  
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 Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile  
 635 640 645  
 Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser  
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Ser Arg Ile

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<212> DNA  
<213> Homo sapiens

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<222> 68, 70, 84, 147  
<223> unknown base

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<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
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Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
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Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
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Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
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His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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 65 70 75  
 His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
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Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser  
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 Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu  
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 365 370 375  
 Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu  
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 Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly  
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 Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe  
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 Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys  
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<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
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Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
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260	265 270
Asp Gly Gly Ala Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln Asn
275	280 285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu Arg
290	295 300
Lys Ile Asn Ala Ala Trp Phe Lys Asn	Met Pro His Leu Lys Val
305	310 315
Leu Asp Leu Glu Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser Gly
320	325 330
Ala Phe Leu Thr Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu Ser
335	340 345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile Ser
350	355 360
Arg Asn Phe Ser Lys Leu Leu Ser Leu	Arg Ala Leu His Leu Arg
365	370 375
Gly Tyr Val Phe Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro Leu
380	385 390
Met Gln Leu Pro Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn Phe
395	400 405
Ile Lys Gln Ile Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn Leu
410	415 420
Glu Ile Ile Tyr Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val Lys
425	430 435
Asp Thr Arg Gln Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg His
440	445 450
Ile Arg Lys Arg Arg Ser Thr Asp Phe	Glu Phe Asp Pro His Ser
455	460 465
Asn Phe Tyr His Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys Ala
470	475 480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe Phe
485	490 495
Ile Gly Pro Asn Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys Leu
500	505 510
Asn Leu Ser Ala Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr Glu
515	520 525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu Asp	635	640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	650	655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	665	670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	680	685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	695	700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	710	715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	725	730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	740	745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	755	760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	770	775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	785	790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	800	805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp  
 815 820 825  
 Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr  
 830 835 840  
 Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp  
 845 850 855  
 Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr  
 860 865 870  
 Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser  
 875 880 885  
 Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu  
 890 895 900  
 Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu  
 905 910 915  
 Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp  
 920 925 930  
 Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val  
 935 940 945  
 Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe  
 950 955 960  
 Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile  
 965 970 975  
 Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu  
 980 985 990  
 Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro  
 995 1000 1005  
 Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn  
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 Asp Ser Ile Lys Gln Tyr  
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- <210> 499
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe



<400> 499  
taaagaccca gctgtgaccg 20

<210> 500  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 500  
atccatgagc ctctgatggg 20

<210> 501  
<211> 45  
<212> DNA  
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<220>  
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<400> 501  
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<210> 502  
<211> 21  
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<220>  
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<400> 502  
gccgagacaa aaacgttctc c 21

<210> 503  
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<212> DNA  
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<220>  
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<400> 503  
catccatgtt ctcatccatt agcc 24

<210> 504  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 504  
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<210> 505  
<211> 1738  
<212> DNA  
<213> Homo sapiens

<400> 505  
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ggctgcaagg gaggtcctcg tggacaggcc aggcaggtgg gcctcaggag 150  
gtgcctccag gcggccagtg ggctgaggc cccagcaagg gctagggtec 200  
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250  
cagcagcatc agcagccccc aggaccgggg aggcacaggt ggccccacc 300  
acccgaggga gcagctcctg cccctgtccg ggggatgact gattctcctc 350  
cgccaggcca cccagaggag aaggccaccc cgctggagg cacaggccat 400  
gaggggctct caggaggtgc tgctgatgtg gcttctggtg ttggcagtgg 450  
gcggcacaga gcacgcctac cggcccggcc gtaggggtgtg tgctgtccgg 500  
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tccagcctgg ccgctgccgc tgccctgcag gatggcgggg tgacacttgc 800  
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gcctgtctgc agacggtaca ctctgtgtgc ccaaggagg gccccccagg 950  
gtggcccca acccgacagg agtggacagt gcaatgaagg aagaagtgc 1000  
gaggtgcag tccagggtgg acctgtgga ggagaagctg cagctggtgc 1050  
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 aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
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 gcccaacttg tttattgcag cttataatgg ttacaaat 1738

<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu	1	5	10	15
Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	20	25	30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu				

	155		160		165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly					
	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala					
	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu					
	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala					
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu					
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu					
	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys					
	260		265		270

Lys Asp Ser

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
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 ccaccatggc cagcctggg ctccagcagc atcagagcag cccctgtggt 150  
 tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttcgcgcta 200  
 cgccctgcgg tgtcccaggg gctgaggtct cctcatcttc tccctagcag 250  
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 gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350  
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60  
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75  
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90  
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105  
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120  
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135  
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
 140 145 150  
 Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
 155 160 165  
 Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
 170 175 180  
 Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
 185 190 195  
 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
 200 205 210  
 Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
 215 220 225  
 Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
 230 235 240  
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
 245 250 255  
 Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
 260 265 270  
 Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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ctgctgcctg acccccagca caataaaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu	
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	
				20					25					30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	
				35					40					45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	



Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
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Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
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Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

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<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 514

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cccgtgggc cggtttatcg ggaggagatt gtcttcagg gctagcaatt 250  
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atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500  
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tcaagaattt ccagataaac aaccagattg tgaaactgaa atactgttac 800  
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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20	25	30
Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile 35	40	45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu 50	55	60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu 65	70	75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp 80	85	90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile 95	100	105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln 110	115	120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile 125	130	135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro 140	145	150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe 155	160	165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn 170	175	180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr 185	190	195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser 200	205	210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr 215	220	225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val 230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr 245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val 260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu 275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly 290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		

	305		310		315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu					
	320		325		330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu					
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Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala					
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Glu Ala Glu Lys

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

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 tttggctttg gactctcnct ttctcccaca gagcncctcg accatcactg 150  
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
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 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 517  
 caacgtgatt tcaaagctgg gctc 24

<210> 518  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtgc cccgtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

gtgcactatt gacaaccggg tcaccgggt ggcctggcta aaccgcagca 350

ccatcctcta tgctgggaat gacaagtgg gcctggatcc tcgcgtggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450  
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<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro	
			20					25						30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
			35					40						45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
			50					55						60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
			65					70						75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
			80					85						90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
			95					100						105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
			110					115						120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
			125					130						135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
			140					145						150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
			155					160						165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
			170					175						180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
			185					190						195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
			200					205						210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
			215					220						225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	
			230					235						240	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
			245					250						255	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
			260					265						270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
			275					280						285	



Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys  
 290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala  
 305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val  
 320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe  
 335 340

<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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 cgtgcgcagc ggagatgcca ccttccccaag agctatggac aacgtgacgg 150  
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<210> 525

<211> 2602

<212> DNA

<213> Homo sapiens

<400> 525

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 tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150  
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 cc 2602

<210> 526  
 <211> 736  
 <212> PRT  
 <213> Homo sapiens

<400> 526  
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 Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu  
 35 40 45  
 Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro  
 50 55 60

Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly	65	70	75
Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp	80	85	90
Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu	95	100	105
Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp	110	115	120
Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu Asn Thr Thr Phe	125	130	135
Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu	140	145	150
Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro	155	160	165
Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly	170	175	180
Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala	185	190	195
Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala	200	205	210
Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser	215	220	225
Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala	230	235	240
Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu	245	250	255
Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met	260	265	270
Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val	275	280	285
Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met	290	295	300
Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu	305	310	315
Glu Phe Leu Ser Phe Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser	320	325	330
Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser	335	340	345

Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile Leu Asn Asn Tyr Leu  
 350 355 360  
 Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser Leu Asp Arg Arg  
 365 370 375  
 Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu Tyr Gly Thr  
 380 385 390  
 Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr  
 395 400 405  
 Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys Ala  
 410 415 420  
 Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile Ser  
 425 430 435  
 Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp  
 440 445 450  
 Met Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp Ala  
 455 460 465  
 Ile Tyr Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys  
 470 475 480  
 Glu Leu Asp Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser  
 485 490 495  
 Phe Phe Gln Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val  
 500 505 510  
 Met Ala Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser  
 515 520 525  
 Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn  
 530 535 540  
 Glu Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala  
 545 550 555  
 Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val  
 560 565 570  
 Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu  
 575 580 585  
 Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser  
 590 595 600  
 Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu Glu Gln Tyr  
 605 610 615  
 Asn Gln Tyr Gln Val Asn Gly Glu Arg Leu Asn Gly Arg Gln Thr  
 620 625 630

Leu Gly Glu Asn Ile Thr Asp Asn Gly Gly Leu Lys Ala Ala Tyr  
 635 640 645  
 Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln  
 650 655 660  
 Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly  
 665 670 675  
 Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His  
 680 685 690  
 Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val  
 695 700 705  
 Leu Gly Thr Leu Ser Asn Ser Arg Asp Phe Leu Arg His Phe Gly  
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 Cys Pro Val Gly Ser Pro Met Asn Pro Gly Gln Leu Cys Glu Val  
 725 730 735

Trp

<210> 527

<211> 4308

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1478, 3978, 4057-4058, 4070

<223> unknown base

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<400> 589  
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<210> 590  
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<210> 597

<211> 25

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<210> 599

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<223> Synthetic oligonucleotide probe

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<210> 605  
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<210> 606  
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<400> 606  
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<210> 611  
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<212> DNA  
<213> Homo Sapien

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accacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200  
ctgtggcgcg ccgcctggtt cccgggaaga ctgccagca ccagggggtg 250  
ggggagtgcg agtgaaagc tgctggagag tgagcagcc tagcagggat 300  
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 tgggacgttt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612  
 <211> 352  
 <212> PRT  
 <213> Homo Sapien

<400> 612

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Ala	Ala	Val	Leu	Leu	Ser	Leu	Cys	Cys	Leu	Leu	Pro	Ser	Cys	Leu
			20						25					30
Pro	Ala	Gly	Gln	Ser	Val	Asp	Phe	Pro	Trp	Ala	Ala	Val	Asp	Asn
			35						40					45
Met	Met	Val	Arg	Lys	Gly	Asp	Thr	Ala	Val	Leu	Arg	Cys	Tyr	Leu
			50						55					60
Glu	Asp	Gly	Ala	Ser	Lys	Gly	Ala	Trp	Leu	Asn	Arg	Ser	Ser	Ile
			65						70					75
Ile	Phe	Ala	Gly	Gly	Asp	Lys	Trp	Ser	Val	Asp	Pro	Arg	Val	Ser
			80						85					90
Ile	Ser	Thr	Leu	Asn	Lys	Arg	Asp	Tyr	Ser	Leu	Gln	Ile	Gln	Asn
			95						100					105
Val	Asp	Val	Thr	Asp	Asp	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr

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Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
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Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu		
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu		
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe		
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln		
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro		
200	205	210
Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile		
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu		
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu Trp		
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile		
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val		
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys		
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr		
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys		
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile Phe Tyr		
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613  
 <211> 1797  
 <212> DNA  
 <213> Homo Sapien

<400> 613  
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ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
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<210> 614  
 <211> 520  
 <212> PRT  
 <213> Homo Sapien

<400> 614  
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 Ile Asn Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser  
 35 40 45  
 Leu Ala Val Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala  
 50 55 60  
 Gly Leu Leu Val Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg  
 65 70 75  
 Val Leu Glu Met Tyr Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp  
 80 85 90  
 Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His Pro Gly Glu His  
 95 100 105  
 Leu Ala Gln Gly Ala Ser Arg Leu Gln Val Leu Gln Ala Gln Leu  
 110 115 120  
 Thr Trp Val Arg Val Ser His Glu His Leu Leu Gln Arg Val Asp  
 125 130 135  
 Asn Phe Thr Gln Asn Pro Gly Met Phe Arg Ile Lys Gly Glu Gln  
 140 145 150  
 Gly Ala Pro Gly Leu Gln Gly His Lys Gly Ala Met Gly Met Pro  
 155 160 165  
 Gly Ala Pro Gly Pro Pro Gly Pro Pro Ala Glu Lys Gly Ala Lys  
 170 175 180  
 Gly Ala Met Gly Arg Asp Gly Ala Thr Gly Pro Ser Gly Pro Gln



185	190	195
Gly Pro Pro Gly Val Lys Gly Glu Ala Gly Leu Gln Gly Pro Gln 200 205 210		
Gly Ala Pro Gly Lys Gln Gly Ala Thr Gly Thr Pro Gly Pro Gln 215 220 225		
Gly Glu Lys Gly Ser Lys Gly Asp Gly Gly Leu Ile Gly Pro Lys 230 235 240		
Gly Glu Thr Gly Thr Lys Gly Glu Lys Gly Asp Leu Gly Leu Pro 245 250 255		
Gly Ser Lys Gly Asp Arg Gly Met Lys Gly Asp Ala Gly Val Met 260 265 270		
Gly Pro Pro Gly Ala Gln Gly Ser Lys Gly Asp Phe Gly Arg Pro 275 280 285		
Gly Pro Pro Gly Leu Ala Gly Phe Pro Gly Ala Lys Gly Asp Gln 290 295 300		
Gly Gln Pro Gly Leu Gln Gly Val Pro Gly Pro Pro Gly Ala Val 305 310 315		
Gly His Pro Gly Ala Lys Gly Glu Pro Gly Ser Ala Gly Ser Pro 320 325 330		
Gly Arg Ala Gly Leu Pro Gly Ser Pro Gly Ser Pro Gly Ala Thr 335 340 345		
Gly Leu Lys Gly Ser Lys Gly Asp Thr Gly Leu Gln Gly Gln Gln 350 355 360		
Gly Arg Lys Gly Glu Ser Gly Val Pro Gly Pro Ala Gly Val Lys 365 370 375		
Gly Glu Gln Gly Ser Pro Gly Leu Ala Gly Pro Lys Gly Ala Pro 380 385 390		
Gly Gln Ala Gly Gln Lys Gly Asp Gln Gly Val Lys Gly Ser Ser 395 400 405		
Gly Glu Gln Gly Val Lys Gly Glu Lys Gly Glu Arg Gly Glu Asn 410 415 420		
Ser Val Ser Val Arg Ile Val Gly Ser Ser Asn Arg Gly Arg Ala 425 430 435		
Glu Val Tyr Tyr Ser Gly Thr Trp Gly Thr Ile Cys Asp Asp Glu 440 445 450		
Trp Gln Asn Ser Asp Ala Ile Val Phe Cys Arg Met Leu Gly Tyr 455 460 465		
Ser Lys Gly Arg Ala Leu Tyr Lys Val Gly Ala Gly Thr Gly Gln		

	470		475		480
Ile Trp Leu Asp	Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu				
	485		490		495
Trp Ser Cys Thr	Lys Asn Ser Trp Gly His His Asp Cys Ser His				
	500		505		510
Glu Glu Asp Ala	Gly Val Glu Cys Ser Val				
	515		520		

<210> 615  
 <211> 647  
 <212> DNA  
 <213> Homo Sapien

<400> 615  
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 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616  
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 20 25 30  
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
 35 40 45

Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp  
50 55 60

Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu  
65 70 75

Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser  
80 85 90

Phe Val Ile Pro Cys Asn Asn Gln  
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<210> 617

<211> 2558

<212> DNA

<213> Homo Sapien

<400> 617

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acagaaattg cttccaagtt cagtgaagaga ctccaggact ttgacaaaag 2150  
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gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250  
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300  
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 gaatccgtat tgaatttgtg tggtatgtca ctcagaaaga atcgtaatgg 2500  
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 atatataa 2558

<210> 618  
 <211> 750  
 <212> PRT  
 <213> Homo Sapien

<400> 618

Met	Trp	Asn	Leu	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Thr	Ala	
1				5					10					15	
Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly	
				20					25					30	
Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser	
			35						40					45	
Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala	
				50					55					60	
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His	
			65						70					75	
Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	
			80						85					90	
Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	
			95						100					105	
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	
			110						115					120	
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	
			125						130					135	
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	
			140						145					150	
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	
			155						160					165	
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	
			170						175					180	
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	
			185						190					195	
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	
			200						205					210	

Gly Asn Lys Val	Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu	485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
500		505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg His	Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu Ser	Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys Val	Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr Val	Ala
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu Val	Ala
740		745	750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

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<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

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<210> 623

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

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<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe



<400> 624

cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50